

SEQUENCE LISTING

```
<1100 Benner, Wolfgang A.
      Barmann, Martin
      Harrick Patrick
       Dermer, Franziska
Cosiel, Peter
       Blossek, Christine
Brossen, Rainer
       10.00, Painer
       Stallenkiel, Matthias
       Frey, Peter
 <!mj \ M. Febular Antigen Array</pre>
 .:.0 - 1761.0190005
 0140 \ 107650,898
0141 \ 11 J-01-18
 . 1540 - MS GC/261,379
.1111 - 11011-01-19
  : 1000 08 60/331,045
: 101 101-11-07
   ... . :atentIn Ver. 2.1
    .:: .::A
.::: A.tificial Sequence
     .... Frimer
                                                                                41
     g:::: megt geageaggta accaeegtta aagaaggeae e
     .[] .2
... 44
... BNA
... Artificial Sequence
     . . primer
      44 . - 2
```

c:: ngttac otgotgoacg ogttgottaa gogacatgta gogg	4 4
<pre>l 3ill .lil .l .l</pre>	
<pre>1</pre>	
-4 - :: -74: prijec tacgatacec	20
.1104 - L11 - 25 - L11 - ENA - L13 - Artificial Sequence	
- Like The Frimer	
ng medi prosetuacy gogogottta caggo	25
WILL ST WILL ST WILL Artificial Sequence	
Primer	
-400 5 	47
-117 - 6 -117 - 40 -118 - DNA -119 - Artificial Sequence	
: Frimer	
; 1 - 8 .:: Trigoty cacgogtyty egytyytegy ategeeegye	40
::	
The Barmer	
.4002 7 gggtotagat toppaaddat toppitatod aggettittig acaabgetat categiotige accagnigge pilitgadade	gataagagaa 60 90

```
K010% 8
KD11 100
KD1, DMA
KD1: Applificial Sequence
  cl.:
C...: :rimer
    principaa ggaggtaaaa aacgatgaaa aagacagcta togogattgo agtggcactg 60
    447 65 5
     portuniting etacograge geaggeette ceaaceatte cettatee
    ould on the state of the state 
        .ii...
.ii. Frimer
                                                                                                                                                                                                                                                                                                                                                                  31
         . 450 - 9
         produstree tagaageeae agetgeeete e
          oul 10
oli 14
oli ORA
oli Artificial Sequence
            · 10.
Ott: Frimer
                                                                                                                                                                                                                                                                                                                                                                        24
               . . . . . 10
              countrygtgg totgadogad accd
                 .... i1
.... 41
.... 5NA
... Artificial Sequence
                  . . Primer
                                                                                                                                                                                                                                                                                                                                                                              41
                     ...---
...: tagaaga gecacegeaa eeacegtgtg eegecaggat g
                   . .; . :- 11
                      .: 12

.:: 33

.:: DMA

.::3 - Artificial Sequence
                           ..( »
...g » Primer
                                                                                                                                                                                                                                                                                                                                                                                  33
                           otatoatota gaatgaatag aggattottt aas
                           . ; ;0> 12
```

```
<210 - 13
×211 · 15
- 12 DNA
- 13 - Artificial Sequence
.3 Modified ribosome binding site
. ::1 1.3
                                                                      15
ajjajjtaaa aaacg
+ 18 14
+ 11 + 21
+ 12 PRT
+ 11 + Artificial Sequence
 _... sagnal peptide
Met. Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -450 \times 14
 In: Wal Ala Gln Ala
              20
   .: 15
 11 46
 PRT
- 113 - Artificial Sequence
 +4 K + 15
 Tys 3ly 3ly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
 Asy Flu Lys Ser Ala Leu Gl<br/>n Thr Glu Ile Ala As<br/>n Leu Lys Glu 25 \, 30 \,
  lys thu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
                               40
  +:11 16
:11 6
+:11 PRT
_:: Artificial Sequence
  Ala Ala Ser Gly Gly
```

```
<010~ 17
. 1 - Description of Artificial Sequence: peptide linker
  4 17
Dly Hy Ser Ala Ala Ala
 + ..1 + + 18
+ 211 + 256
 DDA
- DDA
- DDA
- DDA
   1 3.
1.1 F.3 fusion construct
   - 1 1 - 1 -
  maatilanja ggtaaaaaac gatgaaaaag acagetateg egattgeagt ggeaetgget 60
   ggsttogrta Sögtagogoa ggodtgegtg ggggoggoog oftotggtgg ffgoggfggt 120
   on harogusa seetgeagge ggaaacegas caggtggaag acgaaaaate sgegetgeaa 180
   annyaganeg ogaacotgot gaaagaaaa gaaaagotgg agitcatoot ggoggcacac 240
                                                                                                                                                                                                                                                  256
   ughnutust aagott
  +::: 12
+::: 5.
+::: FFT
+::: Artificial Sequence
   ...ll 
...l
   Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala 5 10
    Gl: Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
    will Ast Sed Lou Lys Clu Lys Slu Lys Len Glu Phe Ile Leu Ala Ala
35 40 45
     H: + Oly Gly Cys
      %L1 : L)
%L11: L61
%L11: LNA
%L13: Artificial Sequence
         ... Fos fusion construct
        _20 +
<221/ CDS
```

```
<2000> 200 .. (240)
ga: ... :: gga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg
                             Met Lys Lys Thr Ala Ile Ala Ile Ala Val
gc = 7 % gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc Ala Lo: Ala Gly Phe Ala Thr Val Ala Gln Aia Cys Gly Gly Leu Thr
ga: act itg cag gcg gaa acc gac cag gtg gaa gac gaa aaa too gcg
As: Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
                                                                                  147
 cti ita acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag
 L. . J.n Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
 this also stig geg gea case ggt ggt tgo ggt ggt tot geg ges get File Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
                                                                                   240
                                                                                   261
  gigtitgggg atatcaaget t
  ..10 - 21
-211 - 73
-211 - ERT
    ii Artificial Sequence
   - 22: Fos fusion construct
   Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
   Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
    The Amp Gla Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
    As: 1-u Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His -1.0
    Bly Gly Cys Gly Gly Ser Ala Ala Ala
    4.1.3 Fos fusion construct
     42202
```

```
<22215 JDS
<...2 - (-1) - (189)
geattiega ggtaaaaaga tatogggtgt ggg god got tot ggt ggt tgo
                                              Ála Ála Ála Ser GĨy GĨy Cýs
gat gat stg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
                                                                                   102
gas asa too gog ctg caa acc gaa atc gog aac ctg ctg aaa gaa aaa G.: Iys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys ... 30
            10
                                                                                   150
day asm ong gag the ate ong gog goa cac ggt ggt tge taagett
Gla Lys Leu Glu Phe Ile Leu Ála Ála His Gly Gly Cys
 - 110 - 13
- 111 - 52
- 112 - FFT
- 113 - Artificial Sequence
  ::::: Fos fusion construct
  Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
   Fly Thr Asp Gin Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
  Ala Ast. Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
  His Biy Gly Cys
   % 10 % 24
% 10 % 204
% 10 % DNA
% 10 % Artificial Sequence
    13 Fos fusion construct
   quatt.bajga gguadaaaac gatggottgo ggtggtotga oogacacoot goaggoggaa 60
    ar georágg tiggaagacga aaaatoogog otgoaaacog aaatogogaa ootgotijaaa 120
    gaaasagaaa agotggagtt catootggog goacacggtg gttgoggtgg ttotgoggoc 180
    dete gigtg gggatateaa gett
    +1210 + 25
+1211 + 56
<2112 PRT
```

```
<213: Artificial Sequence
<.12000
<...3 Eas fusion construct
Lys Th: Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
Asp 71: Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn
                                   25
Lea Lea Lys Glu Lys Glu Lys Leu Gla Phe Ile Leu Ala Ala His Gly
                              40
Gly Tys Gly Ser Ala Ala Ala
55
+ 110 + 16
+ 111 + 16
-213 - 1FI
  PIB - Himb sapiens
\{(4,5),(3,6)\}
Met A.a Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
                                        10
 tys Led Fro Trp Leu Gln Glu Gly Ser Ala
 - 2.11 -
- Fcs fusion construct
 - 401 - 17
 guartinagge etatggetae aggeteeegg aegteeetge teetggettt tggeetgete 60
 typaty mest ggettbaaga gggcagogot gggtgtgggg eggcegette tggtggttge 120
 ngtuntitya organiseet goaggoggaa acegaecang tiggaagaega aaaatoogog 180
  otgomasog amátogogam cotgotgama gamamagama agotggagtt catootggog 240
  grainscriptg gttgetaage tt
  % L1 % L8
% L1 % L2
% L2 % FBT
% L1 % Artificial Sequence
  vimie
vimie Bos fusion construct
  M1. Al. Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gl<br/>n Ala \overline{\mbox{5}}
  Glu The Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Clu Ile
20 25
  Ala Ash Leu Leu Lys Glu Lys Glu Lys Leu Glu Fhe Ile Leu Ala Ala
```

35	40	4.5	
Hi - Gly Gly Cys			
- 17.1			
KOLID 29 FOLID 361 FOLID DNA FOLID Artificial Seq	uence		
Mulle Mile Pos fusion con	struct		
:::			
<pre>cqt() + 20 gwattc atg gct ara :</pre>	ggo too ogg acg Gly Ser Arg Thr 5	tcc ctg ctc ctg go Ser Leu Leu Leu Al 10	t tit ggc 48 a Phe Gly
ota atc tgc ctg dcc Leu Leu Cys Leu Pro	tqg ctt caa ga Trp Leu Gln Gl	g ggc agc gct tgc (u Sly Ser Ala Cys (25	ggt ggt ctg 96 Gly Leu 30
ais gad add otg dag The Asp The Leu Gla 35	gog gaa acc ga Ala Glu Thr As	c cag gtg gaa gac p Gln Val Glu Asp 40	gaa aaa too 144 Slu Lys Ser 45
gry stg saa aso gaa Ala Leu Gln Thr Glu 50	Tie Wie Won no	g ctg aaa gaa aaa u Leu Lys Glu Lys 55	gaa aag ctg 192 Glu Lys Leu 60
gag the atc ctg god The Fre Ile Leu Al: 65	gga cac ggt gg Ala His Gly Gl 70	gt tgc ggt ggt tct ly Cys Gly Gly Ser 75	geg gee get 240 Ala Ala Ala
poptigtggga ggodtaa	gct t		261
.172 30 .112 96 .113 PRT _13 Artificial S	equence		
·.:)· : Fos fusion C	onstruct		
•	5	eu Leu Leu Ala Phe 10	
20		Ser Ala Cys Gly Gly 25	
35	; ~	Val Glu Asp Glu Lys 45	
Gin Thr Glu Ile A	la Asn Leu Leu '	Lys Gla Lys Gla Lys	: Leu Glu Phe

```
60
                      55
    50
II- Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala . 70
+ 1 + 31
+ 11 44
+ 11 DNA
| 117 + Artificial Sequence
.:: Primer
4 0 - 31
                                                             44
.210 - 31
- 111 - 44
- 112 - 1NA
<213 - Artificial Sequence
.270.
.21. F:imer
4 174 8 311
                                                              44
pathanastt caggaggtaa aaagatatog ggtgtggggc ggcc
.1.1.
.113 - Frimer
 4 - 5 - 3
                                                              47
 nytyngaatt caggaggtaa aaaacgatgg cttgcggtgg tctgacc
  . . . rimer
  4 . +4
: mt.mo:gtg gtotgado
                                                               18
  ___/
```

```
<???~ Primer
                                                                       27
<.; . 35
Chinainct tagcaaccac cgtgtgc
::imer
 The lot tgatatooco acacedageg geogragaac cacegeaace aceg
1.4 11 - 34
 Click B"
Click B2
Click BNA
Click Astificial Sequence
 · 115 ·
· ...: · Frimer
                                                                         32
 4.1.7
 constraiget taggeeteee acaeecageg ge
  .M. . H
.M. . H
.M. . MA
.H. Artificial Sequence
  .joi.
.jji. Frimer
                                                                          29
   . 469.558
   propagati caggaggtaa aaaacgatg
   117 - 39
111 - 12
11 - DNA
113 - Artificial Sequence
   :: Frimer
                                                                            32
    .; 1 . 39
    :::::gaatt caggostatg gotacaggot co
    (123> Primer
```

```
27
q: ::::itt catggctaca ggctccc
< .,
. : 11
. :: 13
. :: 1MA
. . : Artificial Sequence
  : Frimer
    .; - : :1
     0.11 0 42
0.111 0 63
0.111 0 187
0.112 0 Art
                        1.875
                       Artificial Sequence
       NITE - Description of Artificial Sequence: Primer
         spraymente ggeactgeen tettgaagee agggeaggea gageaggeea aaageeag
         110 - 43
- 111 - 402
- 112 - EMA
                  ir Artificial Sequence
          .110.
.111.75
.121.(1).(402)
              ato tac doa ggt act dtg tgg tgt ggt dad ggd aad aaa tdt tdt lie Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
             in dog and gan oto ggo ogo tit and one and gad gon tigo tigt ogo my Pro Ash Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
                 The Gar and tot dog gad good and tot got got gad tot add dad the Gar Lys His
                                                                                                                                                                                                                                                                     144
                   13: the act aac acc got tot cac acg ogt etc ago tgo gac tgo ga
                                                                                                                                                                                                                                                                       192
                   ::: aaa tto tas gad tgs oft aag aan too god gat acc ato tot tot
Amp Lys Phe Tyr Asp Cys Leu Lys Ash Ser Ala Asp Thr Ile Ser Sor
65
                     tad the gut ggt ass and tat the sad big alle gat see sas tgt tad
```

```
T_{\lambda}: Phe Val Gly Lys Met Tyr Phe Asn Leu fle Asp Thr Lys Cys Tyr 90
and ctd game cac cod gta acc ggo tgo ggo game cgt acc game ggt cgo
Lys Leu Nu His Pro Val Thr Gly Cys Gly Glu Ard Thr Gly Gly Ard
               100
this ctg sac tac acc gtt gac aaa tot aaa eeg aaa gtt tac eag tgg
Cys Lou His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
                                                                                 384
                                                                                 402
 the gad stg egs aaa tad
 File Asp Leu Arg Lys Tyr
 ._10: 44
._11: 1:4
 ..1. PPT ...1 Sequence
  ....
.223 · Midified bee venom phospholipase A2
   The The Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
  -4(0) \times 44
   Jly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
   Th: Gl: Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His 35
   Bly Leu Thr Asr Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
   Ask Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser 80
   Ty: Fhe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
    Lys Lea Glu His Pro Val Thr Gly Cys G.y Glu Arg Thr Glu Gly Arg
100
    Cys I-u His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp 125 \,
    Ene Asp Leu Arg Lys Tyr
     110 45
      ..11 · 19
      _13 - Artificial Sequence
      0020
8223/ Primer
```

kinne 45 chinista decaggiac	19
46 	
411-46 Nilatatica geggeegegt atttgegeag gteg	34
::;7 .:::::::6 .:::::::::::::::::::::::::::	
gro - 47 rantusttet geggeegeta teatetacee aggtae	36
217 18 : 19 - 112 DNA - 213 Artificial Sequence	
- DE A- - NJB - Primer	
- 400 - 48 - tantatttg ogcaggtog	19
0.11 49 0.11 18 0.11 DNA 0.11 Artificial Sequence	
ii 	
:.A - 49 ::::tccat cggtgcag	18
VII v 50 LII 36 LII DNA LII Artificial Sequence	
((.) Primer	
+ ;:1.+ 50 aubadbadaa goggoogday gggaaabada totgoo	36

```
.l. .
.l. .rimer
                                                                                35
 *..10 * 12
*.11     ..1
*..12     DMA
*..13     Artificial Sequence
. ::
.:: Primer
 +41 1 5D
                                                                                 21
 thallyggaa acadatetge c
 - ..10 - 53
- 211 - 33
- .:12 - ENA
- 213 - Artificial Sequence
 · 11:
· 12 Frimer
  400 53
                                                                                  33
  artaitctag aatgagagtg aaggagaaat atc
  + 110 + 54
+ 111 + 42
+ 311 + 5MA
+ 111 + Artificial Sequence
  ...
[...Primer
  - 41 34
                                                                                  42
  rainstgota geacegaatt tatetaatte caataattet tg
  ...: 55
Li: 51
.... INA
...: Artificial Sequence
  ...
._.: Frimer
  - 1: 12: 55
                                                                                  51
  Mayoa loca ocaaggoaaa gotgaaagot accoagotog agaaabtggo a
```

.210> 56

```
<011> 48
<.! DNA
<.! Artificial Sequence</pre>
... Primer
                                                                               48
Paulinitest attoccacty ecagtitete gagetgggta getiteag
. . . . 56
..13.57

...11.36

...12.5DDA

...13.Artificial Sequence
-....
___? - Primer
                                                                                36
 . 413 - 57
 - 110 - 58
- 311 - 37
- .... FNA
- 113 - Artificial Sequence
 · ....
; <u>:</u> · · Frimer
  8.4
  patricinggo cottaacogo aabcacogtg tgoogoo
  - 110 - 59
- 211 - 46
- 212 - PRT
- 213 - Artificial Sequence
   ....
..... JUN amino acid sequence
   Tys Hy Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys 10 15
   Mia Bin Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
    Tal Ala Glm Leu Lys Glm Lys Val Met Asm His Val Gly Cys
35
    11: 60
11: 46
1: PRT
-:::: Artificial Sequence
```

```
Cy: ... 3ly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu _{\rm 10}
As: 7.1 Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
 Lys the Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys \frac{1}{45}
  *::: * f1
* L11 * f3
* L11 * tNA
* L12 * Artificial Sequence
   . 111: Primer
                                                                                                                                                                                                                                                                                                                                          33
     4.400 \times 61
     congression total transfer to the congression of th
      SCIPS 62
MILS 39
SILS THA
MISS Artificial Sequence
      Primer
        - 4.55 - 62
                                                                                                                                                                                                                                                                                                                                             39
         productable geggeteege aaccaacgtg gtteatgae
        - 110 - 63
- 111 - 50
- 310 - ENA
- 313 - Artificial Sequence
          :21...
:23% Frimer
           properties gageegeggg tagegaeatt gaeeettata aagaatttgg
             1.1. 641.1. 381.1. DNA11. Artificial Sequence
                38
                 . Tritoccae gottotacgg eagogttget eggetegg
```

```
ANG POLY
...: Artificial Sequence
1.26
 ....: Primer
      -55
                                                                               33
 tigg gttgeggtgg teggategee egg
- Dille
Die Frimer
 - 41 - 66
                                                                                38
 ngagarana gettttagea accaaegtgg tteatgae
 1210 - 67
 %311 / 31
%31 / 5NA
%31 / Artificial Sequence
 . _ . . Framer
 - 4 € 7
                                                                                31
  poggaattoa tggadattga oddttataaa g
 - 010 - 68
- 011 - 45
- 010 - DNA
- 011 - Artificial Sequence
  - 11:0
- 11: Primer
  4 1 1 5 6 3
                                                                                 45
  criteriance caaccegege ctageggaag egttgatage atage
   .1 · 69
· L11 · 47
· L12 · DNA
· 11 · Artificial Sequence
   10 .
- 113 - Frimer
   €9
                                                                                 47
   This grate eggtggggge tgeggtggte ggategeeeg getegag
   - 11 - 10
- 11 - 39
- 11 - DNA
    Lis. Artificial Sequence
```

```
~ ; . 70
                                                                              39
q:::::taccc goggotocgc aaccaacgtg gttcatgac
0.1 71
0.11 21
0.11 INA
0.11 Artificial Sequence
14/16/12
                                                                              31
 -_td - 7L
-_t11 - 4%
-_t11 - 5MA
-_t11 - Actificial Sequence
 Dair.
Daire Primer
 4.00 - 7.3
  nijar alog cagoecccae eggatecatt agtacecace caggtage
                                                                               48
  211 - 73
711 - 45
211 - ENA
713 - Artificial Sequence
  4400 - 73
                                                                               45
  gttrantgog gagoogoggg tagogacota gtagtcagtt atgto
  11: 74
11: 56
.II: DNA
.II: Artificial Sequence
  ...:
J.: Primer
   7.4
                                                                                38
   :::::cocaa gottotacgg aagogttgat aggatagg
  +.l + 75
| 111 + 33
| + + + DNA
| +.l + + Artificial Sequence
   .___ Primer
```

```
< 4:10 75</pre>
                                                                    33
(**:: eqcgg gttgcggtgg tcggatcgcc cgg
.11 · '6

.11 · 38

.11 · DNA

.13 · Artificial Sequence
.....
...: Primer
4450 - 76
                                                                     38
 O.11 - 77
O.11 - 30
O.11 - DNA
O.11 - Artificial Sequence
·:lu·
·:lu· Primer
. 439 - 77
                                                                     30
 rograattoa tggccacact tttaaggagc
-110 76
-111 38
217 DNA
 Artificial Sequence
 · L. :
· I. : · Primer
 455 - 78
                                                                      38
 and the case gettttages accasegtgg tteatgac
 . . Primer
 . . . 79
                                                                      31
  Timattoa tggadattga docttataaa g
  _: .
... Primer
  -.:00.- 80
  uctagagosa detitgosas catettetaa attagtaces acceaggiag o
```

```
<.:?> 81
<...: 43
<...: MA
</pre>
...: Extificial Sequence
. :: Frimer
                                                                                            48
isanatugtg gcaaaggtgg ctctagggac ctagtagtca gttatgtc
+ DIN + BD
+ DIN + BF
+ DIN + FNA
+ DIN + Artificial Sequence
 . []. Primer
 32
                                                                                             38
 ninitalnaa gottotaaac aacagtagto tooggaag
 ...11 - 43
-111 - 16
-113 - DNA
-113 - Artificial Sequence
 . 11 ).
.113 - Primer
  44, 53, 33
                                                                                              36
   programtico tagoagotag cacogaatti atotaa
   > 210 + 64
...11 + 33
> 21L + ENA
...13 > Artificial Sequence
  · i.....
· · · !rimer
    ; 14
                                                                                               33
   : itt: a jtcg acatgagagt gaaggagaaa tat
   .: 65

.: 30

.: NA

.: Artificial Sequence
   ::: Primer
                                                                                                30
     :00.2 85
    · waccgaatt caggaggtaa aaagatatgg
     .210> 86
```

```
₹211: 35
...11 - DNA
· :13 · Artificial Sequence
..?).
.:3 - Primer
.:1 - 86
                                                                                35
 : : !taaage ttttaaccac cgcaaccacc agaag
+110 + 87
+11 - 33
+112 + DMA
+711 + Artificial Sequence
 - 135
135 - Primer
 -436 - 87
                                                                                 33
 togaatgage cotcatette gtgtgetagt cag
 0.1100 88
0.111 4
0.111 PRT
 ._13 - Artificial Sequence
 +:117+
+:118+ Fps fusion construct
  4 1 - 83
  3... Phe Arg Arg

0.10 - 89
0.11 - 183
0.10 - SRT
0.13 - Hepatitis B virus

  410 - 89
  Met Ass The Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 10 15
  Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
   The Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
   Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu 50 60
   Let Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile ... 70 75
   Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
   Phe Arg Gin Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
```

			100					105					110		
Glu	Thr	Val 115	Ile	Glu	Туr	Leu	Val 120	Ser	Phe	Gly	Val	Trp 125	Ile	Arg	Thr
Pro	Pro 130	Ala	Туг	Arg	Pro	Pro 135	Asn	Ala	Pro	Ile	L∈u 140	Ser	Thr	Leu	Pro
Glu 145	Thr	Thr	Val	Val.	Arg 150	Arg	Arg	Gly	Arg	Ser 155	Pro	Arg	Arg	Arg	Thr 160
Pro	Ser	Pro	Arq	Arg 165	Arg	Arg	Ser	Gln	Ser 170	Pro	Arg	Arg	Arg	Arg 175	Ser
Gln	Cer	Arg	Gly 180	Ser	Gln	Cys									
·:21	0:- 9: 1:- 1 2:- P: 3:- H	83 RT	itis	В У	irus										
.;40 :4⊖t 1	0: 9 Asp	() Ile	Asp	Pro 5	Туг	Lys	Glu	Phe	Gly 10	Ala	Thr	Val	Glu	Leu 15	Leu
Ser	ihe	Leu	Pro 20	Ser	Asp	Phe	Phe	Pro 25	Ser	Val	Arg	Asp	Leu 30	Leu	Asp
Tnr	Æla	Ser 35		Leu	Туг	Arg	Glu 40	Alâ	Leu	Glu	Ser	Pro 45	Glu	His	Суз
Ser	Fro 50		His	Thr	Ala	Leu 55	Arg	Glrı	Ala	Ile	Leu 60	Cys	Trp	Gly	Glu
Leu 65		Thr	Leu	Ala	Thr 70	Trp	Val	Gly	· Gly	Asn 75	Leu	Gl.u	Asp	Pro	Thr 80
Ser	Arg	Asp	Leu	Val	Val	Ser	Tyr	Val	. Asn 90	Thr	Asn	Met	Gly	Leu 95	Lys
Fh∈	e Arg	; Glr	Leu 100		Trp	Ph∈	Hls	Ile 105	ser	Cys	Leu	Thr	Phe 110	Gly	Ar
Clu	: Thi	: Val		e Glu	г Туг	Leu	ı Val 120	Ser	Ph.e	e Gly	Val	Trp 125	o Ile S	: Arg	Th:
Ero	Pro 130		а Туг	arç	g Pro	Th:	n Asr	n Ala	a Pro	lle	Leu 140	. Ser	Thr	Leu	Pr
(:l: 145		r Cys	s Val	l Ile	e Arç 150	g Arç	g Arç	g Gly	y Arg	g Ser 155	Pro	Arç	g Arg	g Arg	Th 16
Fre	o Se:	r Pro	o Ar	g Arq 165	g Arq	g Ar	g Sei	c Gir	n Ser 170	r Pro	Arq	g Arq	g Arq	g Arg 175	se

Gln Ser Arg Gly Ser Gln Cys 180

- <211> 212
- <::12> PET
- <::13> Hepatitis B virus
- <4000 91
- Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
- Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25
- Asp Fro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
- Pro Sur Asp Phe Phe Pro Ser Val Ang Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glo Leu Met Thr 85 90 95
- Lei Ala Thr Trp Val Gly Gly Ash Leu Glu Asp Pro Ile Ser Arg Asp
- Lei Val Val Ser Tyr Val Asn Thr Asn Met Gly Le: Lys Phe Arg Gln 120
- Let Leu Trp Fhe His Ile Ser Cys Leu Thr Phe Gly Art Glu Thr Val
- lle Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 145 150 150
- Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
- Val Val Arg Arg Arg Gly Arg Ser Fro Arg Arg Arg Thr Pro Ser Pro 180 185 190
- Aig Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
- Alu fer Gla Cys 210
- -:100-92
- .11: 212
- -.12: PRT
- +113 Hepatitis B virus
- 1400 92
- Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 1 5 10
- Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 100 25 30
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 45

- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Sor
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr $90 \ \ 85$
- Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp 100 100
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Fhe Arg Gln 115
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
- Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 150
- Typ Arg Ero Fro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
- Arg Arg Arg Ser Gln Ser Fro Arg Arg Arg Arg Ser Gln Ser Arg
- Clu Ser Gln Dys 210
- .:10 93
- -211: 183 212: PFJ
- 1213 Hepatitis B virus
- Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
- Sar Phe Leu Pro Thr Asp Phe Pro Ser Val Arg Asp Leu Leu Asp 20 20
- Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
- Her Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
- Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
- Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
- Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 100
- Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr

	15				120					125			
Pro Pro A 130	la Tyr	Arg	Pro	Pro <i>1</i> 135	Asn A	Ala	Pro	Ile	Leu 140	Ser 1	Thr I	eu P	ro
Glu Thr C	ys Val	l Val	Arg 150	Arg .	Arg (Gly	Arg	Ser 155	Pro	Arg l	Arg A	Arg T 1	hr 60
Fro Ser P	ro Ar	g Arg 165	Arg	Arg	Ser	Gln	Ser 170	Pro	Arg	Arg	Arg A	Arg S 175	Ser
Oln Ser A	rg Gl 18	u 3er O	Gln	Cys									
.1103 94 .1113 212 .1133 PRO	Γ	s B v	virus										
(40) + 94 (4et Sln) 1	Leu Ph	ne Ris	s Leu	Cys	Leu	Ile	Ile 10	Ser	C7.s	Ser	Cys	Pro 15	Thr
Val Jin	Ala Se	an Lys	s Leu	Суѕ	Leu	Gl y 25	Trp	Leu	Trp	Gly	Met 30	Asp	Ile
Asp Pro	Tyr L: 35	ys Gl	u Phe	Gly	Ala 40	Thr	Val	Glu	ı Lev	Leu 45	Ser	Phe	Leu
Erc Ser 50	Asp P	he Ph	e Pro	Ser 55	Val	Arg	J Asp	Leu	ı L∙∋ı 60	ı Asp	Thr	Ala	Ser
Ala Leu 65	Tyr A	rg Gl	u Ala 70	a Leu	Glu	. S∋ı	Pre	Gl: 7	ı Hi. 5	s Cys	Ser	Pro	His 80
His Thr	Ala I	eu Ar 8	g Gl:	n Ala	a Ile	: Le	а Суя Э(s Tr	p Gl	y Asp) Leu	Met 95	Thr
Leu Ala	Thr I	irp Va	al Gl	y Gly	y Asr	n Le [.]	u Gli 5	u As	p Fr	o Val	l Ser 110	Arg	Asp
Leı Val	Val S 115	Sen Ty	yr Va	l Ası	n Th: 120	r <i>F</i> .s	n Va	l Gl	y Le	ı Ly: 12	s Fh∈ 5	e Arg	Gln
Leu leu 130	Trp l	Phe H	is Il	e Se 13	r Cy 5	s Le	u Ih	r Ph	ie Gl 14	y Ar 10	g Gla	ı Thı	Vai
Ile Glu 145		Leu V	al S∈ 15	er Ph	e Gl	у Уа	l Tr	p II	Le Ai 55	ig Th	r Pro	o Pro	Ala 160
Tyr Arg	g Pro	Fro A	sn Al 65	La Pr	o Il	e L€	eu Se	er Th	nr L	eu Pr	0 Gl	u Thi 175	Thr
Val Val	L Arg	Arg A 180	irg G	ly Ar	g Se	er P: 19	co Ai 35	rg A	rg A	rg Th	ır Pr 19	o Se: 0	r Pro
Arg Arc	g Arg 195		Ser G	ln S∈	er Pr 20	co A DO	rg A:	rg A	rg A	rg Se 2(er Gl 05	n Se	r Arg
Glu Se 21		Cys											

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H:210> 95
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:::11: ...12

-00130 PET

:::13: Hepatitis B virus

(47) DE 95 Met Gla Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val Bla Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile

Asp Pro Tyr Lys Glu Pne Gly Ala Thr Val Glu Leu Leu Ser Phe Leu

Fr: Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His

His Tar Ala Leu Arg Glm Ala lle Leu Cys Trp Gly Asp Leu Met Thr

Low Ala Thr Trp Val Gly Gly Asn Lou Glu Asp Pro Val Ser Arg Asp

Den Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Fhe Arg Gln

ben Leu Tro Fhe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

The Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala

Tyr Arg Pro Fro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 185

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg

Glu Ser Gln Cys 2:10

-1100-96

+ H111+ 212 + 212+ PRT

:213 Hepatitis E virus

+(400 + 96)

Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val Sin Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25 30

- Asp Fro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 40
- Pio Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln
- H:s Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr 85 93
- Leu Ala Thr Trr Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
- Lea Val Val Ser Tyr Val Asn Thr Asn Met Gly Lea Lys Phe Arg Glr.
- Lea Leu Tro Phe His Ile Ser Cys Leu Thr Phe Gly Ang Glu Thr Val
- Ile Glu Tyr Leu Val Ser Pne Gly Val Trp Ile Arg Thr Pro Pro Ala
- Tyr Ang Pro Pro Asn Ala Pro Ile Ieu Ser Thr Leu Pro Glu Thr Thr
- Val Val Arg Arg Arg Gly Arg Ser Fro Arg Arg Arg Thr Pro Ser Pro 185
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg 195 200
- Glu Ser Gln Cys 210
- -1:10: 97
- 211: 212
- 212 PRT
- 213 Hepatitis E virus
- -1400 97
- Met 3ln Leu Phe His Leu Cys Ieu Ile Ile Ser Cys Fer Cys Pro Thr
- 7al 3ln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 -25
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
- Pro Ser Asp Pne Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65 70 80
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Mot Thr 85 90 95
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp

-29-105 100 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val ILG GLU Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Ty: Lys Pro Pro Asn Ala Fro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 195 200 Gly Ser Gln Cys 4.110: 95 .211 - 183 .112 - PFT 1213 Hepatitis B virus Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 15Ser Fhe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp 20 25 30 Thr Ala Ser Ala Leu Fhe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Ary Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro 180 185 Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr 145 150 150

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser 175

Gln Ser Arg Glu Ser Gln Cys 180

40 10: 99

vd 110 183

+1.120+ PF.T

-1.13: Hepatitis B virus

-(4)) → 49

Mat Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 1

Sor Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

Thr Ala Ser Ala Lea Tyr Arg Glu Ala Lea Glu Ser Pro Glu His Cys

Ser Pr: His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asr Met Gly Leu Lys

Ene Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

Glo Thr Val Ile Glo Tyr Leo Val Ser Phe Gly Val Trp Ile Arg Thr

Fro Pro Ala Tyr Arg Fro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro

Thu Inr Thr Val Val Arg Arg Arg Gly Arg Ser Fro Arg Arg Arg Thr

Fro Ser Fro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser

Iln Ser Arg Glu Ser Gln Cys .∂≎

-:10: 100

-111: 212

+0:12: PES

:213: Hepatitis E virus

:400 - 100

Met 3ln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 1 5

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35

- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Lei Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65 70 80
- His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr $85 \,$
- Lei Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp 100 105
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 115
- Let Iou Trp Phe His Ile Ser Cys Leu Tnr Phe Gly Ang Glu Thr Val 130 140
- Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 145 150 150
- Tyr Ang Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 165 170 175
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 185 190
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg 195 200 205
- Glu Ser Gln Cys 210
- .:1::-101
- 1111 212
- ...1. PRT
- 11: Hepatitis E virus
- Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Fro Thr 1 5
- 7al Gln Ala Ser Lys Leu Cys Ieu Gly Trp Leu Trp Asp Met Asp Ile 20 30
- Asr Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
- Frc Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser 50
- Ala Leu Phe Arg Asr Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65 70 75 80
- His Thr Ala Leu Ard Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr 85 90
- Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp 100 100
- Led Val Val Ser Tyr Val Ash Thr Ash Met Gly Led Lys Phe Arg Gln

125 120 115 Lou Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val 130 Ilo Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala 140 150 150 Ty: Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 2:00 Glu Ser Gln Cys 2.10 ·1.100-102 - 211: 183 .010 > PRT 1.13 Artificial Sequence Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 1 1 1 1Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Der Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 105 Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr 145 150 150 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser 175 Gln Ser Arg Glu Ser Gln Cys 180

*-:*21) - 103

-11.11 - 21.2

:::13 - PET

(21 · Hapatitis E virus

Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val Glr Ala Ser Lys Leu Cys Leu Gly Tro Leu Trp Gly Met Asp Ile

As: Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu

Fro See Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His

His Th: Ala Leu Arg Gln Ala Ile Leu Cys Trr Gly Asp Leu Met Ser

Lea Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp

Led Val Val Ser Tyr Val Asn Thr Asn Met Gly Led Lys Phe Arg Gln 125

Leu leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala

Tyr Aig Pro Fro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 165

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro

Arj Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg

Gli Ser Gln Cys 210

.11.: 104

.: 11:- 183

-L17 PRT
-L13 Hepatitis B virus

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 10 15

- Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
- Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
- Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
- Leu Men Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
- Ser Ary Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
- Pho Ary 3ln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 105 1(0)
- Glu Thr Val Ile Glu Tyn Leu Val Ser Phe Gly Val Trp Ile Arg Thr
- Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro 135
- Gli Thr Thr Val Val Arg Arg Gly Arg Ser Fro Arg Arg Arg Thr
- Fro Ser Pro Arg Arg Arg Arg Ser Sln Ser Pro Arg Arg Arg Ser

Oln Ser Arg Glu Ser Gln Cys 180

- · : 1() · 135
- -211: 183
- ...12: PRT
- 213 Hepatitis B virus
- Met Asp Ile Asp Fro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 1 5 10 15
- Ser the Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp 20
- Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
- Ser Fro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
- leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
- Jer Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
- Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 105
- Glu Thr Val Ile Glu Tyr Leu Val Sor Ehe Gly Val Trp Ile Arg Thr

115	120	125
Pro Pro Ala Tyr Arg Pro Pro	Asn Ala Pro Ile Leu 140	Ser Thr Leu Pro
Glu Thr Thr Val Val Arg Arg		
115		
Pro Ser Pro Arg Arg Arg Arg 165	Ser Gln Ser Pro Arg 170	175
Gln Ser Arg Glu Ser Gln Cys 180		
<pre><pre></pre><pre></pre><pre></pre><pre>11 < 1</pre> <pre></pre> <pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre></pre><pre><td></td><td></td></pre></pre>		
(400 + 106 Met Asp Tle Asp Pro Tyr Ly 1		
Ser Phe Leu Pro Ser Asp Ph 20	2.0	
Th: Ala Ser Ala Leu Tyr Ar 35	4 -	
n de la companya de		
Len Met Thr Leu Ala Thr T:		
Ser Arj Asp Leu Val Val S 85		
Phe Ary Gln Leu Leu Trp P 100		
G.u The Val Ile Glu Tyr I	10	
GL. Thr Thr Val Val Arg i		
Fro Ser Pro Arg Arg Arg . 165	Arg Ser Gln Ser Pro A 170	arg Arg Arg Arg Ser 175
Oln Ser Arg Glu Ser Gln 180	Cys	
-(10:-107 -(11:-212 -:::12 PRT -(213) Hepatitis B virus		

<4005-107 Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 10 $^{-10}$ Val Glr Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 45Prc Ser Asp Phe Fhe Pro Ser Val Arg Asp Leu Asp Thr Ala Ser 50 50 Ala Le. Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 6° 70 70His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Gl: Leu Met Thr 85 Le: Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 105 Led Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 115 Let Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Ang Glu Thr Val Ile Clu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Fro Pro Ala Tyr Arg Fro Fro Asn Ala Fro Ile Leu Ser Thr Leu Fro Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 180 180 Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln Cys 2.10 .:1(m-108 -.11 - 212 + D10 + PFT
+ D10 + Hepatitis B virus Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr Val 31n Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser 50

- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 80
- His Thr Ala Leu Arg Gln Ala Ile Leu Dys Trp Gly Asp Leu Met Thr $90\,$
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 100 100
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 115 125
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Fhe Gly Ang Glu Thr Val 130 135
- Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 145 150
- Tyr A:g Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 175 165
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 180 180
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
- Glu Ser Gln Cys 110
- 210 109
- 211 212
- .212 PFT
- -213 · Hepatitis B virus
- Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr 10 10 15
- Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile $20\,$
- Asy Pro Tyr Lys Glu Phe Gly Ala Tor Val Glu Leu Leu Ser Phe Leu 35
- Pro Ser Asp Fhe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser 50
- Ala Le. Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65 70 80
- His Thr Ala Leu Arg 3ln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr 85
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 105
- Lou Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 120
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

		-38-	
130	135	1 /	10
Ile Glu Tyr Leu Va	l Ala Phe Gli 150	y Val Trp Ile A 155	rg Thr Pro Pro Ala 160
Tyr Arg Pro Pro As	n Ala Pro Il	e Leu Ser Thr L 170	eu Pro Glu Thr Thr 175
Val Mal Arg Arg Ar 180	cg Gly Arg Se	r Pro Arg Arg A	rg Thr Pro Ser Pro 190
	er Gln Ser Pr 20	o Arg Arg Arg A	rg Ser Gln Ser Arg 205
Glu Ser Gln Cys 210			
•:110: 110 •::11 •:212 •::11: PFT •::13 • Hepatitis B	virus		
<pre><:100 > 110 Met Gln Leu Phe F 1</pre>	dis Leu Cys L 5	eu Ila Ile Ser 10	Cys Ser Cys Pro Thr 15
Val Gln Ala Ser I 20	Lys Leu Cys I	eu Gly Trp Leu 25	Trp Gly Met Asp Ile
Asr Pro Tyr Lys (Glu Phe Gly A	ala Thr Val Glu 40	Leu Leu Ser Phe Leu 45
50	JJ		Leu Asp Thr Ala Ser 60
6 -	70		His Cys Sar Fro His 80
	80		Gly Glu Ieu Met Thr 95
100		1,0	Pro Ile Ser Arg Asp 110
115		1.20	· Leu Lys Fhe Arg Gln 125
130	100		Gly Arg Glu Thr Val
1 ; 5	12/		
	100		r Leu Prc 3lu Thr Thr 175
187	J		g Arg Thr Pro Ser Pro 190
Arg Arg Arg Arg 195	g Ser Gln Ser	Pro Arg Arg Ar 200	g Arg Ser Gln Ser Arg 205

```
Glu 3er Gln Cys
   2:10
.21: 111
+211 + 212
+211 + 212
+212 + PRT
+211 + H-patitis B virus
- MASURE
- DOD - 13
- DOB - Kaa may be any amino acid.
Me: 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 Val Blr Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
 As: Pro Tyr Lys Glu Fhe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
 Fr. Ser Asp Phe Phe Pro Ser Val Arg Asp Ieu Leu Asp Thr Ala Ser
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
 Let Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
  Lou Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Fhe Arg Gln
                             120
  Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
  Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Tnr Pro Fro Ala
  Typ Arg Fro Pro Asn Ala Pro Tle Leu Ser Thr Leu Fro Giu Thr Thr
                   165
  Wal Wal Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
                                     185
  Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Thr Gln Ser Arg
   Mu Ser Gln Cys
       210
    11() 112
    :::11: 212
   -::11::- PRT
   (213) Hepatitis B virus
```

-40-Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25 Asp Pro Tyr Lys Glu Phe Sly Ala Thr Val Slu Leu Leu Ser Phe Leu 35Pro Ser Asp Phe Fhe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser 50 50 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
60 70 75 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr 85 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 105 Leu Vai Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Fhe Arg Gln 115 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val lie Glu Tyr Leu Val Ser Phe Gly Val Trr Ile Arg Thr Pro Fro Ala 145 150 160 Tyn Arg Pro Fro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr 165 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 185 Arg Arg Arg Ang Ser Gln Ser Fro Arg Arg Arg Arg Ser Gln Ser Arg 195 Glu Ser Gln Cys 210 -_1(: 113 - 1111 212 -1212 - PET :213 · Hepatitis F virus Met 3ln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 1 15 Val 31n Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25

Asp Pro Tyr Lys 31u Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 45

Pro Ser Asp Phe Phe Pro Ser Val Aig Asp Leu Leu Asp Thr Ala Ser 50

- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Fro Glu His Cys Ser Pro His 65 70 80
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Frp Gly Glu Leu Met Thr 90 95
- Lei Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 115 120 125
- Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val $130\,$
- Ile Slu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
- Typ Arg Fro Fro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr
- Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 180 185
- Arg Arg Arg Ser Gln Ser Fro Arg Arg Arg Arg Ser Gln Ser Arg

Glu Ser Gln Cys 1.10

- ...10 114
 ...11 212
 ...12 PRT
 ...213 Hepatitis E virus
- Met 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
- 7al 3ln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val. Glu Leu Leu Ser Fhe Leu
- Fro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65 70 75
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 100
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 115
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

13	0				1	.35					140					
Ile G. 145					150					100						
Tyr Ar	g Pi	ro P	ro A	Asn <i>i</i> 165	Ala E	Pro ∶	Ile I	Leu	Ser 170	Thr	Leu	Pro	Glu	Thr 175	Thm	
Val Va	i A:	rg A	rg 2	Arg	Gly A	Arg :	Ser I	Pro 185	Arg	Arg	Arg	Thr	Pro 190	Ser	Pro	
Arg Ar	ng A 1	rg <i>P</i> 95	Arg	Ser	Gln :	Ser	Pro 1 200	Arg	Arg	Arg	Arg	Ser 205	Gln	Ser	Arg	
Glu Fr 21	o: G 10	ln G	Суз													
+ 2100+ + 2110+ + 2120+ + 2130+	212 PET		tis	B vi	rus	•										
<400 > Met G 1	115 ln I	je a p	Phe	His 5	Leu	Cïs	Leu	Ile	Ile 10	Ser	Cys	Ser	Cys	Pro 15	Thir	
Val 3	ln A	Al.a	Ser 20	Lys	Leu	Cys	Leu	Gly 25	Trp	Leu	Trp	Gly	Met 30	Asp) Ile	
Asp P) 10 (Tyr 35	Lys	Glu	Fhe	Gly	Ala 40	Thr	Val	. Glu	ı Leu	Leu 45	ı S€:1	r Ph∈	e Leu	
Pro S	Ser A	Asp	Fhe	Phe	Pro	Ser 55	Val	Arg	Asp	Leu	Leu 60	Ser	Thu	c Ala	a Ser	
Ala I 65	ie u	Tyr	Arg	Glu	Ala 70	Leu	Glu	Ser	Pro	5 Gli 7.	u His 5	з Суз	s Sei	r Pr	O His	
His :	Γł.r	Ala	Leu	Arg 85	Gln	Ala	lle	Lei	ı Су: 91	s Tr	p Gl	y Gli	л Г-э.	u Me 9	t Thr 5	
Leu i	A_ā	Thr	Trp	. Val	. Gly	val	. Asn	Let 10	ı Gl	u As	p Pr	o Al	a Se 11	r Ar O	g Asp	
Leu	Val	Val 115	Sei	- Туз	: Val	_ Asr	120	As:	n Me	t Gl	y Le	з Бу 12	s Ph 5	e Ar	g Gir.	
	Leu 130	Trp	₽'n€	e His	s Ile	e Ser 135	r Cys 5	s Le	u Th	r Ph	ne Gl 14	y Ar O	g Gl	u Th	r Val	
Ile 145	Glu	Tyn	Lei	ı Va.	1 Se:	r Phe	e Gly	y Va	l Tr	p II	le Ar 55	g Th	r Fr	10 Pi	o Ala 160	à)
Tyr	Arg	Frc	Pr	o As 16	n Ala	a Pr	o Ile	e Le	u Se	er Th	nr Le	u Pr	to G1	lu Th 1	ir Th: 75	r
Val	Val	Arq	g Ar 18	g Ar O	g Gl	y Ar	g Se	r Pr 18	ro Ai 35	cg A:	rg Ar	g Th	nr P:	ro S. 90	er Pr	0
Arg	Arg	Arg 195	g Ar	g Se	r Gl	n Se	r Pr 20	o Ai 0	g A:	rg A	rg Ai	rg Se 20	er G 05	ln S	er Ar	g

Glu Ser Gln Cys 210

<d210: 116
<d211: 212
<d212: PRT
<d213: Hepatitis B virus</pre>

<400 - 116

Met Gla Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu -40 -45

Fro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser

Ala Leu Tyr Ang Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr

Led Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp

Low Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln

Let Let Trp Fhe His Ile Ser Cys Let Thr Phe Gly Arg Glu Thr Val 135

Ite Ghu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Fro Pro Ala

Tyr Arg Fro Fro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 200

Glu Ser Gln Dys 110

110 117 - 211 - 212 - 212 - PRT

Met Gln Leu Pho His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr ·:400 · 117

- Val Gin Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr 85 90
- Leu Ala Thr Trr Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Ph: Lys Gln
- Lea Leu Trp Fhe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
- Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 150
- Tyr Arg Fro Fro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 170
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 135
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 200
- Glu Ser Gln Cys 210
- 2100-115
- 211:- 212
- 213 PRT
- -213 Hepatitis B virus
- $+1400 \cdot 118$
- Het 31n Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
- Val 31n Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 25
- Asp Prc Tyr Lys Glu Pho Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
- Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 65
- His Thr Ala Leu Arg Gin Ala Ile Leu Cys Trp Gly Glu Leu Met Thr

				85					90					95	
L÷u	Ala	Thr	Trp 100	Val	Gly	Th.r	Asn	Leu 105	Glu	Asp	Pro	Ala	Ser 110	Arg	Asp
I.e.a	Val	Val 115	Ser	Tyr	Val	Asn	Thr 120	Asn	Me:	Gly	Leu	Lys 125	Phe	Arg	Gln
I.e ı	Leu 130	Trp	Ph⊹	His	Ile	Ser 135	Cys	Leu	Thr	Phe	Gly 140	Ang	Glu	Thr	Val
Leu 145	Glu	Туг	Leu	Val.	Ser 150	Phe	Gly	Val	Trp	Ile 155	Arg	Thr	Pro	Pro	Ala 160
T)r	Arg	Pro	Pro	Asn 165	Alā	Pro	Ile	L∙∍u	Ser 170	Thr	Len	Pro	Glu	Thr 175	Thr
Val	Val	Arg	Arg 180	Arg	Gly	Arg	Ser	Pro 135	Arg	Arg	Arg	Thr	Pro 190	Ser	Pro
Arg	1.rg	Arg 195	Arg	Sen	Gln	Ser	Pro 200	Arg	Arg	Arg	Ang	Ser 205	Gln	Ser	Arg
Glu	Ser 210	Gln	Суз												
1	0:- 1 1:- 1 2 - P 3 - H	93 F.T	itis	È V.	irus										
:::0 :::t 1	0 + 1 Asp	19 Ile	Азр	Fro 5	Tyr	Lys	Glu	Phe	Gly 10	Ala	S∈r	M∈t	Glu	Leu 15	Leu
Ser	Phe	Leu	Pro 20	Ser	qsA	Phe	Туг	Ero 25	Ser	Val	Arg	Asp	Leu 30	Leu	qzA
Thr	Ala	Ser 35	Ala	Leu	Tyr	Arg	Gl u 40	Ælā	Leu	Glu	Ser	Pro 45	Glu	His	Cys
Tnr	Pro 50		His	Thr	Ala	Leu 55	Arg	Glrı	Ala	Ile	Leu €0	Cys	Trp	Gly	Glu
1.90 65		Thr	Leu	Ala	Thr 70	Trp	Val	GLY	Gy	Asn 75	Leu	Gln	Asp	Pro	Thr 80
Ser	Arş	ı Asp	Leu	. Val 85		Ser	Tyr	Val	Asn 90	Thr	Asn	M⊕t	Gly	Leu 95	Lys
₽h€	e Arç	g Glr	n Lesu 100		. Trp	Phe	His	7al 105	Ser	Cys	Leu	Thr	Phe 110	Gly	Arg
Glv	ı Th:	r Val		. Glu	Tyr	Leu	. Val 120	Ser	Phe	gly	· Val	Trp 125	Ile	e Arg	Thr
Pro	Gl:		a Tyr	r Arç	, Pro) Pro	Asn	Als	a Pro) Ile	Leu 140	Ser	Thr	: Leu	Pro
Gl: 14:		r Cy:	s Val	L Val	Arç 150	g Arç	g Arg	: Gl	/ Arç	g Ser 155	Pro	Arç	, Arç	g Arq	Tr.r 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser 170

Gln Ser Arg Gli Ser Gln Cys

+:210:- 120

-::11: 183

-:..12:- PFT

-1213 - Repatitis B virus

(4)) 1.20

Met Asp lle Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu

3-r The Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr

Ser Ang Asp Leu Val Val Ser Tyr Val Asm Thr Asm Met Gly Leu Lys

Fhe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

Giu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr

Fro Erc Ala Tyr Arg Pro Pro Asn Ala Pro Ile Ieu Ser Thr Leu Fro 135

31d Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr 1.45

Fro Sex Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser 165 170 175

Gln Ser Arg Glu Ser Gln Cys 180

-11):-111

- 11I:- 212

-112 PET

713 · Hepatitis B virus

-:400 - 121

Met 3ln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 - 25 - 30

- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Lei Tys Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr 85 90
- Leu Ala Thr Trp Val Gly Val Ash Leu Glu Ask Pro Ala Ser Arg Asp
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln 125
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val 1:0 135 140
- Ile Siu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Fro Pro Ala
- Tyr Ang Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 180 135
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 195 200 205
- Glu Ber Gln Cys _ 1.0
- 110 122
- 211 212
- D12 PPT D13 Hepatitis B virus
- Met Jin Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
- 7al 31r Ala Ser Lys Leu Jys Leu 31y Trp Leu Trp Gly Met Asp Ile 20 25 30
- Asr Prc Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35
- Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 80
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Mot Thr $85\,$
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp

			100					1	05					1.1	. 0			
Leu V	/al	Val 115	Ser	Tyr	Val	Asn	. Th	nr A 20	sn I	Met	Gly	Leu	Lys 125	Ph	ne A	rg	G1	n
Leu I	Leu 130	Trp	Phe	His	Ile	Ser 135	C:	ys I	.eu	Il∈	Phe	Gly 140	Arç	g Gi	lu T	hr:	۷ā	ì
I.e (Туг	Leu	Val	ser 150	Ph€	; G	ly V	al	Trŗ.	Ile 155	Arg	Tnı	e Pi	ro E	?ro	A1 16	.a 50
Тук	Arg	Pro	Pro	Asn 165	Ala	Pro) I	le 1	Leu	Ser 17	Thr	Leu	Pro	o G	lu [Thr 175	Th	nr
Va. ⊤	Val	Arg	Arg 180	Arg	Gly	Ar	g S	er :	Pro 185	Arg	Arg	Arg	Th	r P 1	ro 90	Ser	Pı	0
Arg	<i>l</i> .rg	Arg 195	Ar:	g Sen	Glr	se	r P	ro.	Ang	Arj	Arg	Arg	Se 20	r G 5	Sl:n	Ser	Α:	rg
Gl.a	Ser	Gln	. Cys	3														
+ 210 + 210 + 312 +313	. · 1	83 F.T	titi	s B '	viru	S												
:40: Met 1	Asp	3 : Il	e As	p Pr	о Ту 5	r L	.'S	Glu	Fhe	G1 ;	y Al	a Th	r Va	al (Glu	Leu 15	1 I	eu
Sər	Ph€	i L∙∋	u Fr 2	o Se O	r As	p Pl	1e	Phe	Erro 25	s Se	r Va	l Ar	g A:	sp	Leu 30	Let	ı F	/sp
Thr	Ala	a Se 3	r Al 5	a Le	u Ts	r A	rg	Glu 40	Ala	a L≕	u Gl	u Se	r P	ro 45	Glu	Hi:	s (Cys
Ser	· Pr 5	c Hi	s Hi	s Th	ır Al	a L	eu 55	Arg	Glr	n Ai	a Il	e Le	eu C 50	ys	Trp	Gl	У	Asp
Leu 65	ı Me		ır Le	eu Al	а Т	nr T 70	rp	Val	Gl;	y Va	l As	sn Le 75	eu G	lu	Asp	Pr	0	Val 80
Ser	: Ar	ą As	sp Le	eu Va 8	al V 35	al S	er	Tyr	Va	1 A.s	sn Ti 90	nr As	sn V	al	Glv	, Le 9	u 5	Lys
Ph∈	e Ar	g Gl	ln L	eu Le 00	eu T	rp E	he	His	; Il 10	e 24 5	er C	ys L	eu T	hr:	Phe 11	e Gl	У	Arg
Glı	u Th	ir V. 1	al I 15	le G	lu T	yr I	Leu	Val 120	Se	r I	ne G	ly Λ	al :	Erp 125	Ile	e Ar	g	Thr
Pr	c P:	:5 A	la T	yr A	rg F	ro '	Pro 135	Ası	n Al	.a P	ro I	le L 1	eu : 40	Ser	Th	r L	eù	Pro
Gl 14	L T		hr V	al V	al <i>F</i>	rg . .50	Arg	ar:	g Gl	y A	rg S 1	er F	ro.	Arg	Ar	g A.	rg	Thr 160
		er P	ro P	Ala <i>A</i>	rg <i>F</i> .65	Arg	Arç	g Se	r G	ln S 1	er E 70	ro P	rg	Arg	, Ar	g A 1	rg 75	Ser

Gln Ser Arg Glu Ser Gln Cys 180

<2105 134

HE111 212

:212> PRT

4213.4 Hepatitis B virus

Met 31% Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

Val 31r. Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25 30

As: Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu -45

Se: Asp Fhe Phe Fro Ser Val Ary Asp Leu Leu Asp Thr Ala Ser

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Fro His

His Thr Ala Leu Ary Gln Ala Ile Leu Cys Trr Gly Asp Leu Met Asn

Let Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp

Lea Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln 115

Lou Lou Trp Phe His Ile Ser Cys Lou Thr Phe Gly Arg Glu Thr Val 135

The Glu Tyr Leu Val Ser Phe Gly Val Trp He Arg Thr Pro Pro Ala

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 200

Gla Ser Gln Cys 210

-210> 125

-211: 183 :212: PET

4313 Hepatitis B virus

Met Asp Ile Asp Prc Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 10 15

- Ser Phe Leu Pro Ser Asp Pho Phe Pro Ser Val Arg Asp Leu Leu Asp
- Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
- Ser Fro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
- Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
- Ser Ary Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
- Phe Ang lin Leu Leu Trp Pho His Ile Sen Cys Leu Thr Phe Gly Ang 105
- Gla Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
- Fro Fro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser The Leu Pro
- Glu Ter Thr Val Val Arg Arg Arg Gly Arg Thr Fro Arg Arg Arg Thr 150
- Pro Ser Fro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser 170
- Glr. Ser Arg Glu Ser Gln Cys 130
- -00100 106 -011 212 -012 PFC

- .113 · Hepatitis B virus
- Met Glr. Leu Fhe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Tar (40) 126
- Val 31n Ala Ser Lys Leu 3ys Leu 31y Trp Leu Trp Gly Met Asp Ile 20 30
- Asp Frc Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 40 45
- Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
- His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr 85 90
- Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 100 105
- Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln

120 115 Ile Lou Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 3lu Thr Val 135 1:0 Ile Guu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr 170 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Fro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln Cys 110 <210 · 127 -1.11 · 212 -212 > PET · 213 · Hepatitis B virus Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 7al 31n Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile 20 25 Asp Pro Tyr Lys Glu Fhe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35 Fro Ser Asp Fhe Phe Fro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 80 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr 35 90 Le: Ala Thr Trp Val Gly Val Asn Ieu Glu Asp Pro Ala Thr Arg Asp 100 100 Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Ehe Arg Gln 115 \$120Let Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val 135 Il- Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 14. 150 155 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 175 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 185 Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg 195

Glu Cer Gin Cys

<0.10 + 123
<011 + 212
<011 + PFT</pre>

212 Heratitis E virus

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr 10 15

Val 31n Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp 31y Met Asp Ile 25

Asr Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 40° 35°

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser 50

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 6: 75

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr 90 95

Let Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp 105

Let Val Val Ser Tyr Val Asn Thr Asn Met Gly Let Lys Phe Arg Gln 115

Le: Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val 130 135

Il- 3lu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala 150 150

The And Pro Pro Ash Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 185

Ang Ang Ang Ser Gln Ser Pro Ang Ang Thr Ang Ser Gln Ser Ang 195

Glu Ser Gln Cys (10

- 210 - 129

- 211 - 212 - 212 - PRT

.213 - Hepatitis B virus

4400× 129

- Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr
- Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Aso Ile 20 25
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
- Pro Ser Asp Phe Phe Fro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
- Ala Lei Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
- His The Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr $85\,$
- Lei Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp
- Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln $120\,$
- Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
- Lou Giu Tyr Lea Val Ser Phe Giy Val Trp Ile Arg Thr Pro Pro Ala 150
- Tyr Aug Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Fro Glu Thr Thr
- Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
- Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
- Glu Ser Gln Cys 110
- +210: 130 +211: 212
- 212 PFS Hepatitis B virus
- Met 3ln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
- Val 3ln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asr Ile 20 25
- Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu 35
- Pro Ser Ala Phe Pne Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser 50 60
- Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His

		٠.		
	5	75		80
65 His Thr Ala Leu Arc	70 - cin Ala Il	e Leu Cys Trp G	ly Asp Leu Met 95	Thr
His Thr Ala Leu Arg	1 91.1 7.2	90	ro Ala Ser Arg	Asp
Leu Ala Thr Trp Va	i Gly Val As	in Leu Gla Asp 1 105	110	Gln
Leu Val Val Ser Ty	r Val Asn T	hr Asn Met Gly I 20	Leu Lys Phe Are 125	
Tou Jeu Trp Phe Hi	is Ile Ser C	ys Leu Thr Phe	Gly Arg Glu ^{Thi} 140	r vai
13° Ile Glu Tyr Leu V	al Ser Phe (Sly Val Trp Ile	Arg Thr Pro Pr	o Ala 160
Tyr Ary Pro Pro P	150	Tie Leu Ser Thr	Leu Fro Glu Th	r Thr
Tyr Arj Pro Pro A	asn Ala Pro 165	170	Ara Thr Fro Se	er Pro
Val Val Arg Arg 18)	Arg Gly Arg	Ser Pro Arg Arg 185	190	- m Ara
And Arg Arg Arg	Ser Gln Ser	Pro Arg Arg Arg 200	Arg Ser Gin S 205	er Arg
Glu Ser Gln Cys 210				
:010 : 101 :011	B virus			Tou
<pre><40>> 131 Met Asp Ile Asp</pre>	o Pro Tyr Ly 5	s Glu Phe Gly A	la Thr Val Glu	15
Ser Pho Leu Pr	o Ser Asp Ph	ne Phe Pro Ser V 25	al Arg Asp Leu 30	Теп изь
ms ri Ala Al	a Leu Tyr A	rg Glu Ala Leu (Glu Ser Pro Glu 45	HIS CYS
35	is Tar Ala I	eu Arg Gln Ala	Ile Leu Cys Try 50	o Gly Glu
Se: P10 M10 W	TIA Thr	Err Val Gly Asn	Asn Leu Glu As	p Pro Ala 80
Le: Met Thr L 61	eu Ala 1112	mar Wai Asn	Thr Asn Met Gl	y Leu Lys
Ser Arg Asp I	eu Val Val 85	Asn Tyr Val Asn 90	Tou Thr Ph	ne Gly Arg
Ite Arg Gln	Leu Leu Trp	Phe His Ile Ser	Cys Leu III 1	io
Glu Thr Val	Leu Glu Tyr	Let Val Ser Pho	Gly Val Trp I	te Aly ****
Pro Pro Ala 130	Tyr Arg Pro	Pro Asn Ala Pro 135	o Ile Leu Ser 1 140	1.1 104 11

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Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
Gln Wer Arg Glu Ser Gln Cys
             180
-110 · 133
 ...11 · 183
 :212 - PFT
 -213 - Hepatitis B virus
 \pm 400 \times 1 \pm 2 Met Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 Ser the Leu Prc Ser Asp Fhe Phe Pro Ser Val Arg Asp Leu Leu Asp 25
  Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
  Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
  Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asr Pro Ile
   Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
   Pho And Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
   Glo Tor Val Tie Glu Tyr Leu Val Ser Phe Gly Val Trp Tle Arg Thr
   Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
   G. Ter Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
    Fro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
    Oln Ser Arg Gly Ser Gln Cys
                  180
     :10 · 133
:11 · 3221
      _13 DNA
      11: Hepatitis B virus
     + .21 CDS
-22. + (1901) .. (2458)
     <4002 133
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ttocactgon ttocaccaag etetgoagga edecagagto agyogtotgt atritoctge 60 tggtggctch agttcaggaa cagtaaachd tgctccgaat attgcctctc acatctcgtc 12) aatotoogo; aggactgggg accortgtgac gaacatggag aacatcacat caggattoot 18) aggaecocty etegtettae aggegggett titatigtty acaagaatee teacaatace 24) geagagteta gaetemiggi ggaettethit caattitata gggggateae eegigigiet 300 tggocaaaat tojoajtopo caapptooka toactoappa acotoptgto otocaattig 3(0) teotogttat ogstgjatgt gretgeging tittateata tiestotica teotgetget 4.) atgeotrate thattating that cause attacas sign at q to q to q to q at q to q to q to q at q at q to q at asttocagja toaacaalaa boagtacqgg accatgbasa acctgcacga otoctgotba (4) aggrametet augusteset caugusgetg tacmamment acquetggma attgements (0) tattescate coatigiset gggettinge aaaataeeta tgggagtggg eetbagtesg $\epsilon \in \mathbb{C}$ titetettgg eleagittae tagigeeatt tgitteagigg tiegtaggge titteecedae 1.0 tgtttiggott toagotatat ggatgatgtg gtattiggggg ocaagtotgt acagcatogt 780 gagtocottt atacogityt techaatttt ottttytoto tyggtataca tttaaacoot 840 aabaaaaaaa aaaqatgggg ttattoodta aabttbatgg gttabataat tggaagttgg 200 ggaacattgo racaggatoa tantgtabaa aagatbaaab abtgttttag aasacttoot (Θ_i) gttaacaggo otastgattg gasagtatgt caaagaattg tgggtotstt gggottsgot 1020 geteratita racaatgigg atatoriged thaaigeett tgtatgeatg talacagget 1080 aaacaggott toactttoto godaacttad aaggoottto taagtaaada gtabatgaad 1140 etttaeseeg tigetoggea aeggeetggi etgigesaag igittgetga egeaacseen 1100 actigating going geometric aggreen aggreen and consider 1360cogatocata otypogyaact pitagoogot tgtattgoto goagooggto tggagosaa; 132) otoatoggaa otjacaatto tytogtooto togoggasat itabatogtt topatogotj 1380 otaggstgta otgonaactg gatoottogo gegacytoot tijtttacgi obegingges 1440 otgaatooog oggangaddo ototoggggo ogottogggad totatogtoo pottotoogt 1500 etgoogtton andojaceae ggggggdadd tetetttacg oggtetedde gtotgtgent 1940 teteatotg: eggteegtgt geaetteget teacetetge aegttgeatg gagastaceg 1620 tgaacgooda toagatootg occaaggtot tacataagag gactottgga otoocaagcaa 1680 totcaacgas cgaccitgag goctactica aagastgigt gittaaggac igggaggagc 1740 tgggggagga gattaggtta aaqqtotttg tattaggagg otqtaggcat aaattggtot 1800 gogoaccago accatgoaac tetetoacce otgoctaato atdeotegta catgedocac 1860

tgttcaagcc tccaagctgt gccttgggtg gctttggggc atg gac att gac cct 1915 Met Asp Ile Asp Pro	
1	
tat aaa kaa ttt gga mot act gtg gag tta ctc tog ttt ttg cct tct 1963 Tyr Lys Tlu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser 10	
gad the itt dot too gto aga gat obe oba gad add god toa got obg 2011 Asp Phe Phe Pho Ser 7al Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu 30 35	
tat oga jaa goo tta jag tot oot gag oat tyd toa oot dad oat act 2150 Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr	à
goa ot; agg caa go; att ot; tgc tgg ggg gaa ttg atg act cta got 200 Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala 60	7
acc tgg gtg ggt aat aat ttg gaa gat coa gca tcc agg gat cta gta 115 Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val 85	5
gto aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg = 200 Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu 95	:3
tgg tit cat ata tot tgc oft act tit gga aga gag act gta oft gaa - 200 Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu 105 - 110	1
tat tig gid ton thi gga gig tigg att ope abt dot doa god tat aga = 11 Tyr Leu Val Ser Fhe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg 120 = 125	39
coa coa aat goo cot ato tta toa aca out ong gaa abt act gtt gtt 13 Pro Pri Asn Ala Fro Ile Leu Sem Thr Leu Pro Glu Thr Thr Val Val 135	47
aga oga ogg gad oga ggd agg tod det aga aga aga act ded tog det 13 Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro 160	95
	4 3
gaa tut daa tgt tag tattoottqg actbataagg tgggaaabtt tabtgggbtt - 2 Glu Ser Gln Cys 	498
rotto tota cartacitat otttaatoot gaatggcaaa otoottoott tootaagatt 2	558
and the case aggainst that the transfer calcalate the theory of the calculation of the case of the cas	010
monny tagga gatt magatt aattatgoot gotagattot atootagooa caddaaacae .	
thomathag acadaggaat taaasottat tatocagato aggtagttaa toattaotto .	. , 5 5
caaaccagac attatttaca tactotttgg aaggotggta ttotatataa gagggaaacc .	_ / 20

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agqt::gt:a ttaaaacctc gcaaacgcat ggggacgaat ctttctgttc ccaaccctc: 2918
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trapiantic aacoccatea aggaeracty gecageagec aaccaggtag gagtgegage 3038
attraggeda gggeteaebe etecadaegg eggtattitig gggtggagbe eteaggetea 3098
gggratating accaraging caacaattoo tectorings tecaecaate ggeagicaeg 3158
asygragost actorcatot stocarctot aagagaragt catoctcagg coatgragty 3218
                                                                   3221
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 Ser She Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 Th: Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
  Ser Pri His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
                          55
  Les Met Thr Les Ala Thr Trp Val Gly Ash Ash Les Glu Asp Pro Ala
  Ser Ard Asp Leu Val Val Asr. Tyr Val Asn Thr Asn Met Gly Leu Lys
  The Arg Gln Leu Leu Trp Phe His The Ser Cys Leu Thr Phe Gly Arg
  Gid Thr Val Leu Glu Tyr Leu Val Ser Fhe Gly Val Tre He Arg Thr
  Fr: Pr: Ala Tyr Arg Fro Pro Asn Ala Pro Ile Leu Ser Thr Leu Fro
   Gi: Thr Thr Val Val Arg Arg Arg Arg Gly Arg Ser Pro Arg Arg 160
                           1.35
      The Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
   At: Ser Gln Ser Arg Glu Ser Gln Cys
   .jio: 135
   188
12 PF.T
   ...13 Woodchuck hepatitis B virus
   Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
1 15
    Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp 25 30
    Thr Ala Thr Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys
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40
35 Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu 55 60
Leu Th: Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gin 80 65
Val Arj Thr Ile Ile Val Ash His Val Ash Asp Thr Trp Gly Leu Lys 95 85
Val Arg 3in Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln 100
His Thr Val Glu Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr 125
Pro Ala Ero Tyr Arg Pro Pro Asn Ala Ero Ile Leu Ser Thr Leu Pro
Giu His Thr Val Ile Arg Arg Arg Sly Sly Ala Arg Ala Ser Arg Ser 150
Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Ser Gin Ser Pro 175 175
Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys 185
4010 - 136 -211 - 217 -212 - PET -2213 - Ground squirrel hepatitis virus
<400 · 136 Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro 15
1 Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp 25
Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe 45 35
Leu Fro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Va! Asp Thr Ala 60
Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro 70 75
His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr 95 85
Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg 100
Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln 125 115
Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val 130

- Gin Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
- Tyr A:g P:o Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
- Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg 180 180
- Arg Thr Fro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg 200
- Arg Ser Gin Ser Pro Ala Ser Asn Cys
- <:2.10 13 -
- -m11 260
- 3212 · PFT
- <:213 Sr.ow Goose Repatitis 2 Virus</pre>
- Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
- Asp Asp Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp 20
- Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
- lle Ala Thr His Phe Val Asr Leu Ile Glu Asp Phe Trp Gln Thr Thr $50\,$
- Glr. Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro 80
- The The Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
- Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
- Val Ser Phe Glm Bro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
- Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg
- Arg Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr 145 150 150 145
- Val Thr Ash Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
- Lys Tyr Arg Gly Arg Asp Ala Fro Thr The Glu Ala Ile Thr Arg Pro 180 180
- The Gin Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys 195
- Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Mal

215
210 217 Tyr Bly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro 240 230 235
0.15
Gin Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser His His Arg 255 245
Ser Fro Ser Pro Arg Lys 260
+ 21G + 138 + 211
-(40) - 176 Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln 15 1
Gly fle Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu 25 30
Val Cys Thr Ite Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala 45
Ser Arg Ala Leu Ala Asr. Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro 50
Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr 80
Tro Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe 95 85
Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu 100
Ile. Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val 120 125
Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu 135
Giy Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Fro 160 145
Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala 175
Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Ieu Leu Trp Trp 180 185
His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile 200 205
Sor Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys 215
Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu 250 255

PED Arg Arg Arg Val Lys Thr Thr lle Val Tyr Gly Arg Arg Arg 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser

Pro Leu Ero Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg

Glu 305

+1100 - 139 +111 - 211

4012 PEST <213 < Ha-mophilus influenzae</pre>

Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe

Phe Sly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asr Ser Glu $\frac{45}{35}$

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln 50 55

Gly Tyr Thr Ala Met Gln Thr Fro Phe Thr Ile Thr Leu Glu Asn Cys -65

Asn Val Thr Thr Asn Asr. Lys Fro Lys Ala Thr Lys Val Gly Val 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu 100 100

Lys Asr. The Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val 115 $^{-125}\,$

Asi: Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val 130 140

GLY Lys Thr Thr Thr Asp Phe Thr Ser Glu Asr His Asn Gly Ala Gly 145 \$150\$

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu 175

Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala 180 185

Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln 195

Ile Ala Tyr Glu

.10

<400. 142

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<.11. 140
40011 + 123
40012 + EEC
421 - Fraudomonas stutzeri
Met Lyr Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
-:4(:→ 14)
Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
Gl:. Asr Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile $40$
 The Pro-Gly Lys Ile Gly Fhe Glu Gln Ala Ile Asn Glu Gly Lys Thr
 Pr. Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
 Thr Ser Tyr Cys Asp Val Asp Ieu Asp Thr Ala Ala Asp Gly His Ile
85
  (
 Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
  Ile Th: Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
           115
  Let her Ala Lys Tyr Lys Pro Gly Lys Cys Ser
  .110-141
  +111 + 59
+112 + PET
  113 · Caulobacter crescentus
   the Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr 15
   Ala Ne Glu Tyr Sly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val 30
   Inr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys
   Ala Sty Ala Ala Val Ser Thr Ala Ala Gly Thr
    +21 0 142
+210 173
-210 PRT
    4213 - Escherichia coli
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- Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln 15
- Gly 31n Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys \$20\$
- Set The Ser Gln Lys Ser Ala Asp Gln Ser The Asp Phe Gly Gln Leu \$40\$
- Se: Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu 5:
- As: Il-: Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn 6: 75
- Gl; Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val 85
- As: Gly Eis Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala 100 100
- Ile Val "al Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu 125
- Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr 130 $$130\,$
- A.a Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly 145
- Ala Ene Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr 3ln 165
- + 010 + 143 + 011 + 173
- -212 PFI
- 4.113 Escherichia coli
- Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
- Fig. Gir. Gly Lys Val Thr Phe Ash Gly Thr Val Val Asp Ala Pro Cys \$20\$
- Mer Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu \$40\$
- Ger Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu 50
- Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn $\epsilon\epsilon$
- 317 Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val 85
- Ash Gly His Ser Asp Glu Leu Asp Thr Ash Gly Gly Thr Gly Thr Ala 100
- Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu

125 120 115 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr Ala "al Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly Ala Fne Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln 165 -210 - 144 .211 17: -111 - FEST -211 - Escherichia coli Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln Gly Glu Gly Arg Val Thr Phe Ash Gly Thr Val Val Asp Ala Pro Cys \$20\$Ser Ile Ser Gln Lys Ser Ala Asp Gin Ser Ile Asp Phe Gly Gln Leu Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu Asp I.e Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser Giy His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile Met. The Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly 120 Asp Fig Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr Va. Gly Lys Lys Ser Ser Asp Gly Ash Ala Gln Tie Thr Glu Gly Ala 150 155 The Par Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln 165 - L10 145 - .11 - 853 - .12 - LNA . 113 - Escherichia coli .20 · 22.. (281)..(829) acgittetgi ggelegaege atotteetea trottetete saaaaaceae eteatgeaat 60 -:40Jz 145

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ataaacatot ataaataaag ataacaaata gaatuttaag ccaacaaata aactgaaaaa 1	120
and gotgettiac ctctatgagt caaaatggcc ccaatgtill atdividing	
ggaaantgtg cagtgttggc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc :	240
ggaaastgtg dagtgttggd dgwll ggaaagsagd atg aaa att aaa act ccatgtcgat ttagaaatag ttttttgaaa ggaaagsagd atg aaa att aaa act Met Lys Ile Lys Thr 1	295
ctg dea atd gtt gtt. ctg tog got ctg toc ctc agt tot acg acg got Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Ser The Thr Ala 15	343
otg god god god abg gdt aat gdt gdg abb gtt dad tit ama gdg Leu Ala Ala The The Val Ash Gly Bly The Val His Ehe Lys Gly 25	391
gaa gtt gtt aac gcc gct tgc gca gct gat gca ggc tot gtt gat caa Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala Bly Ser Val Asp Gln 40	439
acc gtt dag tta gga dag gtt ogt acc gda tog otg gda dag gaa gga Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly 65	487
goa acc agt tot got gto ggt ttt aac att cag otg aat gat tgo gat Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Glr. Leu Asn Asp Cys Asp	535
acc aat gtt gca tot aaa gco gct gtt gcc ttt tta ggt acg gcg att Thr Asn Val Ala Ser Lys Ala Ala Val Ala Fhe Leu Gly Thr Ala Ile 90	583
gat gog ggt dat acc aas gtt etg get etg dag agt tea get gog ggt Asp Ala Gly His Thr Ast Val Leu Ala Leu Gln Ser Ser Ala Ala Gly 115	631
ago goa aca aac qtt ggt gtg cag atc ctg gao aga acg ggt gct gcg Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asg Arg Thr Gly Ala Ala	679
otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac otg acg otg gat ggt gog aca ttt agt toa gaa aca acc otg aat aac	727
gga acc ast acc att deg tto dag gdg dgt tat ttt gda acc ggg gdd Gly Thr Ash Thr Ile Fro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala 160	775
ge4 acc cog ggt get get aat geg gat geg acc tte aag gtt eag tat Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Glr. Tyr 170 175	823
cas taa cotacctagg ttcagggacg ttca Gln	853

^{%10&}gt; 14€
%11> 182
%12> PR1
%213> Escherichia coli

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Se: Jul Thr Thr Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr 20
Va. H.s Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
Gly See Val Asp 3ln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
Len Ala Bin Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
Let Ash Asp Cys Asp Thr Ash Val Ala Ser Lys Ala Ala Val Ala Phe 90 95
 Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
                 105
 Set Set Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
 Ary Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
 The The Deu Ash Ash Gly The Ash The He Pro Phe Gln Ala Arg Tyr 150
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111 31
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   148
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. [ 1 37
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    primer
    ..... 149
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```
37
q::::gtatg gtgaggtgag gaatgeteag gagaete
37
.400 - 150
 partitioning agreattents acctsaceat actgoac
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*:II *: : : :
*:IL *:INA
*:IR *:Artificial Sequence
 . 110. -
. 213 - primer
                                                                                33
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.010 - 5NA
.013 - Artificial Sequence
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    purpost and attitutions teactiffing and
    . [17 - 154
- .... 281
- .... FRT
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    that Jer Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe 10 15
    Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Aia Ser 25
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- Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
- Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
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- Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala The Ala Pro Asp Ala
- Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
- Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
- Leu Glu Asp Ash Ser Lys Glu Trp Thr Ser Leu Phe Arp Ash Asp Ile 115
- Pro Val Thr Thr Asp Asp Val Sor Leu Ala Asp Lys Ala Ile Glu Ser 130 135
- Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr 145 150 150
- Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr 175
- Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
- Gly Lys Asp Asp Glu Ser Arg leu Asp His Leu Gly Val Val Ala Tyr 195
- Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Fro Glu Ser 210 220
- Sen Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg 215 230 240
- Ang Ser Arg Ala Arg Lys Leu 3ln Arg Met Lys 3ln Leu 3lu Asp Lys
- Val Glu Glu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
- Arg Leu Lys Lys Leu Val Gly Glu Arg
- -:10: 155
- -111 181 212 PRT
- · 213 · Escherichia coli
- Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu 15 10 15
- Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr \$20\$
- Val His Pre Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala

35	40	45	
Gly Ser Val Asp Gln	Thr Val Gln Le	u Gly Gln Val Arg Thr Ala Ser 60	
	Ala Thr Ser Se	r Ala Val Gly Phe Asn Ile Gln 75	
Leu Asn Asp Cys Asp 85	Thr Asn Val Al	a Ser Lys Ala Ala Val Ala Phe 90 95	
Lei Gly Thr Ala Ile 100	Asp Ala Gly Hi	s Thr Asn Val Leu Ala Leu Gln 110	
Ser Ser Ala Ala Gly	Ser Ala Thr As	sn Val Gly Val Gln Ile Leu Asp 125	
Arg Thr Bly Ala Ala	Leu Thr Leu A. 135	sp Gly Ala Thr Phe Ser Ser Glu 140	
145	100	hr Ile Pro Phe Gln Ala Arg Tyr 155	
Fhe Ala Gly Ala Al	a Thr Pro Gly A 5	la Ala Asn Ala Asp Ala Thr Phe 170	
Iys Val Gln Tyr Gl 180	n		
-11C+ 156 -111 447 -111 DMA -113 H-patitis B -120* -211 CDS			
. 222 - (1) (447)			
Met Asp Ile Asp F	ct tat aaa gaa ro Tyr Lys Glu 5	ttt gga gct act gtg gag tta ctc 4 Phe Gly Ala Thr Val Glu Leu Leu 10 15	18
l leg tit litg com t Ser Phe Leu Pro S 20		oot too gta oga gat ott ota gat Pro Ser Val Arg Asp Leu Leu Asp 25	96
	tg tat cgg gat eu Tyr Arg Asp 40	gcc tta gag tct cct gag cat tgt Ala Leu Glu Ser Frc Glu His Cys 45	144
	act gca ctc agg Thr Ala Leu Arg 55	caa gca att ctt tgc tgg gga gac Gln Ala Ile Leu Cys Trp Gly Asp 60	192
	got acc tgg gtg Ala Thr Trp Val 70	ggt act aat tta gaa gat cca gca Gly Thr Asn Leu Glu Asp Pro Ala 75 80	240
	gta gto agt tat Val Val Ser Tyr	gto aac act aat gtg ggo cla aag Val Asn Thr Asn Val Gly Leu Lys	288

95 90 85 tto aga caa tta ttg tgg ttt cac att tet tgt ete aet ttt gga aga Ph. And Sln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 ga, any get one gag tan the gen tot ten gga gig teg att ogo act 384 Ğlı Tnr Val Leu Ğlü Tyr Leu Val Ser Phe Ğly Val Trp Ile Arg Thr 115 cot oca goo tat aga coa coa aat goo oot ato ota toa aog ott oog Fro Fro Ala Tyr Arg Pro Pro Asn Ala Fro Ile Leu Ser Thr Leu Pro 135 447 gag act act gtt gtt Clu Thr Thr Val Val +1100 157 ...11: 149 ...12: FRT Hills - Hepatitis B Met Asr Ile Asr Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Ehe Leu Pro Ser Asp Ehe Phe Pro Ser Val Arg Asp Leu Leu Asp Tor Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Ary Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe A:g Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glo Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr 120 Fro Ero Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro 135 Glu Tnr Thr Val Val -1100-158 -1.11: 152 1.12 · PRT Haratitis B

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Ser Pho Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Gly Gly

Lys Gly Gly Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val

Gly Lau Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr 100 100

Phe Gly Arg Siu Thr Val Leu Slu Tyr Leu Val Ser Phe Gly Val Trp

Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser 130

Thr Leu Pro Glu Thr Thr Val Val 145

+00.100 159 +00.11 + 130 +00.12 + PRT

-1213 - Barteriophage Q Beta

Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val 25

Ala Ser Ieu Ser Gin Ala Gly Ala Val Pro Ala Leu Glu Lys Arj Val

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg lys Asn Tyr Lys Val 50

iln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Jly Ser Cys 80 70

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu 100 100

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu 125

Asn Pro Ala Tyr

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·221.25
+22130 - Basteriophage R 17
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Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
 Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
 Ang Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
 Pro Lys Vai Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
 Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
 Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
 Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
                             120
  T \in \mathtt{I}
  -213 - Bacteriophage fr
  .(400> 161
  Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
  Gly Asp Val Lys Val Ala Pro Ser Asn Fhe Ala Asn Gly Val Ala Glu
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   Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser ^{35}
   Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
50 55
   ValProLysValAlaThrGlnValGlyValGluLeuProVal50707580
   Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
85
   Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
100 100
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Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly 120 115 Ile Tyr 130 #2110 162 #2110 130 #2110 PRT H213 - Basteriophage GA (4) 1 - 162 Me. Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly 10 As: Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp Le: Ser Asr. Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr Ary Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val Pr: Lys Tle Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala 85 Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe Tyr Ala 130 . [] 00: 163 -L11:- 132 ...2 - PRI -213 - Bacteriophage SP .4)0 - 163 Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly 10 15 Asp 31r. Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg 35 40 45 Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys 50

Val Gin Ile Lys Leu Gin Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys

75 7.0 65 Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe The Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu Asn Ero Ala Tyr +0100 164 +0110 130 +012 PET .::3 - Bacteriophage MS2 -:400 - 164 Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Tro Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val Fro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val 65 70 75 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Let Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Die Tyr 130 - 100- 165 - 111: 133 - 112: PRT - 113 - Bacterlophage M11 Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly 10 15 Asp Val Thr Leu Asp Leu Ash Pro Arg Gly Val Ash Pro Thr Ash Gly 25 Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg

Val Thr lle Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys

Val 31n Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr 65

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser 90 95

Pho Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu

Lei Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn

Leu Asn Pro Ala Tyr 130

.212 PRT .213 Bacteriophage MX1

Met. Ala Lys leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg

Val Thr lle Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr 65 70 75

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Fhe Ser

Phe Thr Glr. Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu 100 100

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn 120

Leu Asn Pro Ala Tyr 130

· 100 167

.211: 330

::12: PRT

:213: Bacteriophage NL95

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- Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg 35
- Val Thr Val Ser Val Ala Sln Pro Ser Arg Asn Arg Lys Asn Tyr Lys 50
- Val Glr. Ile Lys Leu Gln Asr. Pro Thr Ala Cys Thr Lys Asp Ala Cys 65
- Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe 85
- Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu 105
- Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu 115
- Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly 130 135
- Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro 145
- Gly Gly Thr Gly Thr Tyr Arg Cys Fro Phe Ala Cys Tyr Arg Arg Gly $170 \,$ $165 \,$
- Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys 180
- Gly Ser Glu Ala Leu Val Glu Ehe Glu Tyr Ala Leu Glu Asp Phe Leu 195 \$205\$
- Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp 210 $$ 210
- Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp 240
- Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp 250 245
- Val Val Lys Met 3ln Pro Pro 3ly Thr Phe Asp Ser Fro Arg Tyr Tyr 260 ..70
- Leu His leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu 7al Thr Ala 275
- Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser 290
- Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro 305
- Val Gln Thr Val Ile Val Ile Pro Ser Leu 330

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Th: His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His 35

Gly Lea Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp 55

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser 61

Ty: Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr 90

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg 100 105

Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp 115

Fhe Asp Leu Arg Lys Tyr

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The Ile Tyr Fro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser 10 15

Cly Pro Asn Olu Leu Gly Arg Phe Lys His Thr Asp Ala Cvs Cys Arg 25

Thr His Asr Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His 35

Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asr Asp Leu 50 60

The Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys 75

Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro 85

Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr 105

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Tyr

.2175 170

·:211 ·:..12 134

PRT

1213 - Apis dorsata

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Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg $\frac{25}{20}$

Se: Hi* Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His 35

Gly Lei Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp 50

Asy Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser 75

Tyr Fhe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr 90 95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg 100

Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr 3ln Trp 125

Fire Asp Leu Arg Lys Tyr

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. 11 - 134

-112 - PET -13 Apis cerana

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Dry Pro Ash Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg 25

The His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His 35

:ly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp 50

Asp Thr Fhe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser 75

Tyr Phe Mal Gly Lys Met Tyr Phe Ash led Ile Asp Thr Lys Cys Tyr

35 Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg 105 Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp 125 Ene Asp Leu Arg Lys Fyr 130 <111 · 172 -211 13€ +011 + PRT Bombus pennsylvanicus The Ile Tyr Pro Gly Thr Leu Trp Cys Gly Asn Gly Asn Ile Ala Asn 15 Gly Th: Asn Glu Leu Gly Leu Trp Lys Glu Thr Asp Ala Cys Cys Arg 20 25 Thr His Asp Met Cys Pro Asp Ile Ile Glu Ala His Gly Ser Lys His 35 Gly Lea Thr Asr. Pro Ala Asp Tyr Thr Arg Lea Asn Cys Glu Cys Asp 50 51: Gli Phe Arg His Cys Leu His Ash Ser Gly Asp Ala Val Ser Ala 55 70 80 Als Fhe Val Gly Arg Thr Tyr Phe Thr Ile Leu Gly Thr Gln Cys Phe 85Arg Leu Asp Tyr Pro Ile Val Lys Cys Lys Val Lys Ser Thr Ile Leu 105 Arg 3lu Cys Lys 3lu Tyr Glu Phe Asp Thr Asn Ala Pro Gln Lys Tyr 125 $\,$ 125 $\,$ Gin Trp Fhe Asp Val Leu Ser Tyr 130 135 .2100 173 142 ...12 PRT Heloderma suspectum - _13 Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala 10 15 Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys \$25\$Cys Arg Asp His Asp His Cys Ser Asp Thr Met Ala Ala Leu Glu Tyr \$40\$Lys His Gly Met Arg Asn Tyr Arg Pro His Thr Val Ser His Cys Asp

50
Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Asn Val Lys Asp Arg Thr 75
Ala Asp Leu Val Gly Met Thr Tyr Phe Thr Val Leu Lys Ile Ser Cys
Prie Thu Leu Glu Glu Gly Glu Gly Cys Val Asp Ash Ash Phe Ser Gln 105
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Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
Tys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr 80
Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys 95
Phe Blu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu 100 105
G.1 Jys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Sor Ala 125
Ala Fro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg 135
- 0100 - 175 - 110 - 142 - 013 - PRT - 013 - Heldderma suspectum
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Cys Arı Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr 40 45

Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp 55

Cys Asp Asn 3ln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr 75

Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys 85

Phe Hu Leu Glu Glu Gly Clu Gly Cys Val Asp Trp Asn Phe Trp Leu 100

Glu Dys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala 125

Ala Ero Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly 130 135

###105 176 ###115 574 ###11.5 PFT

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Asp Ser Tyr Ile His Trp Ile Arg 3ln Ala Pro Gly His 3ly Leu Glu 50

Tro Val Cly Tro Ile Asr. Fro Asn Ser Gly Gly Thr Asn Tyr Ala Pro 65

Ang Phe Gln Gly Arg Val Thr Met Thr Arg Asp Ala Ser Phe Ser Thr 90 95

Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Asp Asp Ser Ala Val Phe 100 100

Tyr Cys Ala Lys Ser Asp Pro Phe Trp Ser Asp Tyr Tyr Asn Fhe Asp 115

Tyr Ser Tyr Thr Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val 130 135

Ser Ser Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys 145 150 160

Cys Lys Asn lle Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu

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Ser Lei Ash Gly Thr Thr Met Thr 200	Leu Pro Ala Thr Thr Leu Thr Leu 205
Ser Gly His Tyr Ala Thr Ile Ser	Leu Leu Thr Val Ser Gly Ala Trp 220
Ala Lys Gln Met Fhe Thr Cys Arg	Val Ala His Thr Pro Ser Ser Thr 240
225 Asp Trp Val Asp Ash Lys Thr Phe 245	
	Ser Ser Cys Asp Gly Gly His 165
Phe Fro Pri Thr Ile Gln Leu Leu 275	Cys Leu Val Ser Gly Tyr Thr Pro
	Glu Asp Gly Gin Val Met Asp Val
	Gln Glu Gly Glu Leu Ala Ser Thr 320
Glr. Ser Glu Leu Thr Leu Ser Gl	n Lys Eis Trr Leu Ser Asp Arg Thr 335
Tyr Thr Cys 31r Val Thr Tyr 31	n Gly His The Phe Glu Asp Ser Thr 350
Lys Lys Cys Ala Asp Ser Asn Pr 355	cc Arg Gly Val Ser Ala Tyr Leu Ser 365
Arg Pro Ser Pro Phe Asp Leu Pi 370	ne Ile Arg Lys Ser Pro Thr Ile Thr 380
Cys Leu Val Val Asp Leu Ala P 335	r: Ser Lys Gly Thr Val Asn Leu Thr 400
Top Ser Arg Ala Ser Gly Lys F 405	r) Val Asr. H.s Ger Thr Arg Lys Glu 410
Glu Lys Glr Arg Asn Gly Thr I 420	Leg Thr Val Thr Ser Thr Leu Pro Val 435
Gly Thr Arg Asp Trp Ile Glu (435	Gly Glu Thr Tyr Glr. Cys Arg Val Thr 440 450 Thr Lys Thr Ser
His Pro His Leu Fro Arg Ala 450	Lau Met Arg Ser Thr Thr Lys Thr Ser 46)
Gly Pro Arg Ala Ala Pro Glu 465	Val Tyr Ala Phe Ala Thr Pro Glu Trp 480
Pro Gly Ser Arg Asp Lys Arg 485	Thr Leu Ala Cys Leu Ile Gln Asn Phe 490

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Gly the Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu (1)
Gln Ly3 Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
 Ser Gin Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
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    The Ash His Arg Gly Tyr Trp Val
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111 IgE Mimotype
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     :::u> 130
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0011% 10
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    CD10 - 185
CD11 - 10
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CD13 - IgE Mimotype
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                            5
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.111 - 10
.111 - PRT
.11 - IgH Wimotype
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- 211> 10
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Leu Leu Asp Ser Arg Tyr Trp
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FILE PRT
FILE IGE Mimotype
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                        .3108 132
.311 7
.211 PRT
.311 IgE Mimotype
                             Her top Gly Met Gln Gly Arg
                               193

15

15

PRT

112 IgE Mimotype
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L11> 9
K212> PRT
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 .3165 136
.115 56
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^{-211 - 5464} -213 - DNA

CL13 - PFIMAICEFG

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atggcatgae agtaagagaa ttatgeagtg etgecataae catgagtgat aacaetgegg	610
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otggogaast asttastota gottosoggo aasaattaat agastggatg gaggoggata	847
aagttgoagg accaettety egotegyees tteeggetgg etygtstatt getgataaat	9.701
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octooogtat ogtagttato tadaqqaqqq qqaqtqaqqq aactatggat gaaqqasata	1020
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-104-	
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ttogacoayo ggutathhta ahhhoyotga tacaacatac aqtogaatga atogctacaa	6.74.0
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618) cagnatotica cacquictica acquicquat gaccaatotig gotquitgiat acqqitacqit 624 getigaligas aacaacetna getatagegt geaaacegge tatgeegggg gaggegatigg aaatagngga agtacagget aegreacget gaattatege ggtggttaeg geaateenaa 63() tatoggitae agecatajog atgutattaa geagotetat taeqqaqtea geggtqqqjt 63() 6 actigoricat godaatggog taabgolggg goagoogtta aabqataogg tiggtgootigt €4- takagogoot ggogokaasg atgokaaaagt ogaakaccag acgggggtgo gtaccgaotg gogtggttat googtgotgo ottatgread tyaatatogg gaasatagag tggogotgga 6541 66.0 taccaatane otggotgala acglogatti agataacgog gitigotaacg tigiticceao $i \in \dots$ togtogggig atogtgogag cadaqtttaa agogogogtt gogataasac tgotcatgac (5.7.1) gotgauddad aataataa;; pg:tgddgtt tgg;gbgatg gtgacatda; agagtaguda gagtagogge attgttgogg ataatggtca ggtttacote agoggaatgo etttagoggg $p_{i} = 1$ aasagttoag gtgaaatggg gagaagagga aaatgotoab tgtgtogoda attatosast 5640 godardagag agtoagoago agttattaao ocagotatoa gotgaatgto gttaaggggg ι<u>ς</u> (11... ogtgatgaga aasaaacett tttatsstet ytgegetitt ttytygetyg egytyagtsa 6960 egetttgget geggatagea egattastat segeggetat gtragggata aeggetgtag 7000 7::3 tgtggccgct gaatcaacca attttactgt tgatctgatg gaaaacgcgg cgaagcaatt taaraacatt ggogogalga diootgttgt topatttogt attitigetgt caccetgtgg 5140 7:14.0 taatqoogit toigoogiaa aqqtiqqqit taoigqogii qoaqataqoo acaatqocaa $\mathbb{C}(\mathbb{C}(\sqrt{n}))$ cotgettgoa ettgaaaata eggtgteage ggottoggga etgggaatae agettotgaa tgagbagbaa aatoaaatae esettaatgo tebatogtoe gogetttogt ggabgabeet 73-23 7330 gadgoogggt aaaccaaata ogotqaattt ttacgoocgg claatggoga cabaggtgoo ngticactigog giggoatatica atgebacgge tacetteact ettgaatate agtaactigga 7440 gardonialg assigned assigned trustingsog grastatingg ogciogosag 7500 1 - (1) tgojacgata paggna mog atgicaddat bebaggigaad qqitaaqqiog icdocaaadd ~77.0 gtgtabggtt todabdica atgbrædggt tjætdtoggd sætdtttætt etstdægtot tangtotgod ggggoggoat oggootggoa tgabyttgog ottgagttga otsantgtod ggtgggaaeg tegagggtea stgccagstt cageggggea (segasagta eeggatatta tasaaaccag gygaccgcgc aaaasatoca gttagagota saygatyaca ytygsaacac 74.10 7340 atigaatact ggcgcaacca aaasagttca ggtggatgat testcasaat sagegcaett drzgttacag gtdagagdat tgadagtaaa tggdggagdz adtdagggaa odattdaggd 7920 agtgattago atcacitata octacagotg aaicegaaga gatgattgta atgaaacgag 7980

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traffancot gittgetgia eigelgaigg geiggieggi aaaigeeigg teatiegeei
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tyllaria: otggogttac ccaacttaat egeettgeag cacateeece tttegeeage
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                                                                    8400
cognitives acgoingacgo goodigacgg gottglotgo toocggoato egettacaga
cargotita orginicog gagetgeatg tgteagaggi titeacegie ateacegaaa
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                                                                     8464
 C^{-1}
Gys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
 .010 - 208
.011 - 13
 % II. FFC
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 .400 - 208
 Cys Gly Gly Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
  . 216 × 209
 1460 × 109
  Ala Ala Ala Ser Gly Gly Cys Gly Gly
  211 · ...10
-...11 · ...145
  +21... FET
+11... PLA2 fusion protein
  thet Ala Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys
   Jul Ser Cly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys
    Tys Arj Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser
35
   Lys His Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp
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50 Cys Asp Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys Met Tyr Fhe Asn Leu Ile Asp Thr Lys Cys Tyr Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu 105 Gly Arg Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr 115 120 125 Gin Trp Phe Asp Leu Arg Lys Tyr Ala Ala Ala Ser Gly Gly Cys Gly 130 135 Gl7 145 <213> Ce4mimotope - :00 - 2.11 Gly Glu Fre Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro Ala +210 + 210 +211 + 37 +212 + PRT 212 · Synthetic M2 Peptide <400 · 212 Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys Arg Tys Asn Gly Ser Ser Asp Gly Gly Cys 20 410 → 213 Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys Arq Cys Ash Gly Ser Ser Asp Pro Leu Ala Ile Ala Ash Ile 20 25 The Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe 35Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser 50 55

42

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The Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gin
Gin Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
Gili
+210 + 1.14
+111 + 42
+212 + 2NA
. 11 . Oligonucleotide
×460 × 314
tsacugaatt daggaggtaa aaacatatgg ctatcatcta cc
×210 × 215
-111 - 123
-112 - PRT
 -213 Barteriophage f2
 <400 · 215
 Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
 Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
 lle Sen Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
 Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
 Fro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala 80
  Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala 35
  In: Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu 105 110
  Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
                               120
  151
  +1.100 1.16
+1.110 17
+1.120 FRT
  -:400 - L16
   Gly Glu Phe Cys Ile Asn His Ard Gly Tyr Trp Val Cys Gly Asp Pro
1 10 15
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Ala

<pre>40108</pre>
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lys 3ln Thr Leu Val Leu Asn Pro Arg 3ly Val Asn Pro Thr Asn Gly 20 25
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Val Thr Val Ser Val Ser Gln Pr> Ser Arg Asn Arg Lys Asn Tyr Lys 50
Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser 80 65
Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser 85
Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu 100 105
Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln 100 115
Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Gly Ser Gly 130
Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro 160 145
Gly Thr Gly Lys Tyr Thr Cys Fro Phe Ala Ile Tro Ser Leu Glu Glu 175
Val Tyr Glu Pro Pro Thr Lys Asn Ary Pro Trp Pro Ile Tyr Asn Ala 193
Val Glu Leu Gln Fro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu 195 200 205
Sly Asr. Thr Lys Trp Arg Asr Trp Asp Ser Arg Leu Ser Tyr Thr Thr 2.0
Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr 240 235
Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu 255 245
Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu 260 265

Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His

285 280 ...75 Ala Asp Sly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Sly Gly 295 Ala lle Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile 320 Gln Ala Val Ile Val Val Pro Arg Ala 3.25 .110: 118 .211: 70 -212 · FRT +213 + Amyloid-Beta Protein (Homo Sapiens) 1100 - 118 Met Leu Pro Bly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg Ala Leu Glu Val Fro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro Ille Ala Met Fhe Cys Gly Arg Leu Asn Met His Met Asn Val Gln Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp Thr Lys Glu Gly lle Leu Gin Tyr Cys Gln Glu Val Tyr Pro Glu Leu Gln Ile Thr Asn Val Val Glu Ala Asn Gln Fro Val Thr Ile Gln Asn 90 -95Try Cys Lys Arg 3ly Arg Lys Gln Cys Lys Thr His Pro His Phe Val $100\,$ The Fro Tyr Arg Cys Leu Val Gly Glu Fhe Val Ser Asp Ala Leu Leu 125 \$125\$Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile Asr Lys Phe Arg Sly Val Glu Fhe Val Cys Cys Pro Leu Ala Glu Glu Ser Asp Asr. Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val 195 Trp Trp Gly Gly Ala Asp Tnr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu

230 235 240)
Glu Ala Asp Asp Glu Asp Glu Asp Gly Asp Glu Val Glu Glo 255	J
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Il 26)	е
Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Ar 275 28)	
Glu Val Cys Ser Glu Sln Ala Glu Thr Gly Pro Cys Arg Ala Met Il 290 295	
Ser Arg Trp Tyr Phe Asr Val Thr Glu Gly Lys Cys Ala Pro Phe Ph 305 316 316	
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Ty 335	
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys T 340	
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Tor Thr A 365	
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly A 370 375	
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu A	
Lys His Arg Glu Arg Met Ser Glr Val Met Arg Glu Trp Glu Glu A 405	
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val 420 420	
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala 445 435	
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala 450 460	
Leu Asn Asp Arg Arg Leu Als Leu Glu Asn Tyr Ile Thr Ala 475	
Gln Ala Val Fro Fro Arg Pro Arg His Val Phe Asn Met Leu Lys 495	
Tyr Val Arg Kla Glu Gln Lys Asp Arg Gln His Thr Leu Lys His 500 500	
Glu His Val Arg Met Val Asr Pro Lys Lys Ala Ala Gln Ile Arg 525	
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln 535 540	
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Glr 545 - 550	1 Asp 560

- Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val 565 570
- Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala 530 590
- Leu Met Pro Ser Leu Thr Gla Thr Lys Thr Thr Val Glu Leu Leu Pro 5)5
- Val Asn Gly Glu Pne Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe 610 615 620
- Gly Ala Asp Ser Val Pro Ala Ash Thr Glu Ash Glu Val Glu Fro Val 625 630 635
- Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Sec 645
- Gly Lea Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp 660 665
- Ala Glu Fhe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu 675
- Val Fhe Fhe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly 690 700
- Lea Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Lea 705 710
- Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val 735
- Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met $740 \\ 745$
- Gln Gln Asr Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met 765 765

Gln Asn 770

- .<u>11</u>00--219
- 8 E 18 18 <u>-</u> 1
- 113: Beta-Amyloid Peptide Frequesor (Homo Sapiens)
- <400 → 219</p>
- Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys
 1 10 15
- Mat Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val Eis His Gln 25
- Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile 35
- Ile Gly Lou Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile 50 55

Thm Ieu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val 75 75 80

val Glu

-t210H 2.)

:211: 4-:212: PET

4213 - Amyloid Beta Peptide

(400 - 21.)

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys 1

Leu Val Fhe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile $20 \ 25$

Gly Leu Met Val Gly Gly Val Val Ile Ala

<210> 221

.2115 149 .2125 FRT

+213 Homo sapiens

4400 - 221

Tyr Phe Arg Ala Gln Met Asp Fro Asn Arg Ile Ser Glu Asp Gly Thr 10 15

His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln 20 25 30

Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys 35

Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln 50 55

His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp 65 70 75

Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro 85

Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Sor His 100 105

Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile 115 120 125 Ser Asn Met Thr Phe Ser Asn Gly Lys Leu lle Val Asn Gln Asp Gly 1.30

Ph: Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser 150 14

Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys

Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser 185

Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn

Val Gly Gly Phe Fhe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu

Val Ser Ash Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe

Cly Ala Fhe Lys Mal Arg Asp Ile Asp 345

+010: 000 +010: 044 +010: PET

- 213 - Homo sapiens

-:400> 222

Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr Arg

Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu

Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln 4.0

Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser

Gln His Ile Ard Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp

Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr

Ile Asn Ala Thr Asp Ile Pro Ser Gly Sor His Lys Val Ser Leu Ser 100

Ser Trp Tyr His Asp Ar; Gly Trp Ala Lys Ile Ser Asn Met Thr Phe 115

Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr

Ala Ash Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr

Glu Tyr Leu Gln Leu Mot Val Tyr Val Thr Lys Thr Ser Ile Lys Ile

Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser 180

Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe 200

Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser 110

Leu leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val 235 230

Arg Asp Ile Asp

+.21C+ 443 +.211+ 447 +.212+ 5RT -213+ Mus musculus

-:40) - 323

Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr

His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln

Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg

Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile 55

Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser 65

Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala

His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val 105

Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn

Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr 130 155

Ty: Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser

Va. Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser 165

The Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys 185

Ash Tip Ser Gly Ash Ser Glu Phe His Phe Tyr Ser Ile Ash Val Gly 195

Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser 215

Asn Fro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 230

Fine Lys Val Glin Asp Ile Asp 245

< 21(d) 224

+111+ 199 +310+ PET

-213 - Mus musculus

1100 224

Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile

Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser

Trp Leu Asp Val Ala Gin Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala 35

His Lau Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val 50 60

Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn 80

Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr $90 \ \ 85$

Tyr Leu Tyr Ala Asr. Ile Cys Phe Arg His His Glu Thr Ser Gly Ser 100 100

Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser 115

Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys 130

Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly 145 150

G!y Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gin Val Ser 165 170

Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 180 180

Fine Lys Val Gln Asp Ile Asp 195

+1100 225

.1.11: 114

- 215: PF.T

211 Rattus sp.

(400 - 225

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu 10 15

Sly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 20 25

Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr 35

Phe Ser 3ly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr

Fre Ala

<2105 22€

+211+ 114 +212> PET

<013> Mus musculus

<400 > 226

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu

Sly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 25

Fre Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr

Phe Ser Gly Thr Ash Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Giy Lvs Tle Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Cys $\frac{31}{57}$

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile

Ash Tyr Tyr Asp Met Ash Ala Ala Ash Val Gly Trp Ash Gly Ser Thr 100

Fhe Ala

+..10> 227 +::11> 114 +:212> PRT

<213> Homo sapi∈ns

<400 . 227

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp

Gly Ph. Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys

Fro Pr: Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala

Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys

Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile

As: Tyr Tyr Asr Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr

Fire Ala

(400 - 228

Mot Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Ser

Leu Slu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly

Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn

Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser

Asp Tyr Tyr Asn Arg Ser Th: Ser Fro Trp Asn Leu His Arg Asn Glu 65

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His

Lea Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His 115

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys

Thr Cys Val Thr Pro Ile Val His His Val Ala 150

<21C> 229
+011> 158
<012> PRT

<213 Mus musculus

<400 ← 229

Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu

Leu Ser Leu Ala Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Glr. Ser

Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys

Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg

Ard Pro Ser Asp Tyr Leu Asn Ard Ser Thr Ser Pro Trp Thr Leu His

Arj Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln

Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His 100

Met Asn Ser Val Leu Ile Glr. Gln Glu Ile Leu Val Leu Lys Arg Glu

Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly 130

Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala 150 145

<0.10> 230
 <0.11> 132
 <0.11 FRT</pre>

1211 - Homo sapiens

.:401- .:30

Met Ala Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly

Phe Ala Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu 20

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys

As: Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys

Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu

Lys Tr.r Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala $90\,$

Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala 100

Gln Phe Val Lys Asp Leu Leu His Leu Lys Lys Leu Phe Arg Glu

31; Ard Phe Asn 130

. [10: 231

112 112 112 PRT 113 Homo sapiens

-:400 → 231

Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu

Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met

Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu

Ser leu 11e Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg

Met Lau Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser

Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys

Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Fhe Asn 1.05 100

<010 + 032
+011 111
+011 + PFT
+0213 Mus musculus</pre>

<400 - 2.32

Gly Pro Val Pro Arg Ser Val Ser Leu Pro Leu Thr Leu Lys Glu Leu

Ilo Glu Glu Leu Ser Asn Ile Thr Gln Asp Gln Thr Pro Leu Cys Asn

Gly Ser Met Val Trp Ser Val Asp Ieu Ala Ala Gly Gly Phe Cys Val

Ala lei Asp Ser Leu Thr Asn Ile Ser Asn Cys Asn Ala Ile Tyr Arg

The Gin Arg Ile Leu His Gly Leu Cys Asn Arg Lys Ala Pro Thr Thr

Val Ser Ser Leu Pro Asp Thr Lys Ile Glu Val Ala His Phe Ile Thr 85

Lys Leu Leu Ser Tyr Thr Lys Gln Leu Phe Arg His Gly Pro Phe

+ 1101 233 + 111 134 + 112 + PRT + 113 + Homo sapiens

-:400 233

Met Arg Met Leu Leu His Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr 1 5 10

Val Tyr Ala Ile Pro Thr Glu Ile Pro Thr Ser Ala Leu Val Lys Glu 20 25 30

Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu Leu Ile Ala Ash Glu 35 40 45

Thr Leu Arg Ile Pro Val Pro Val His Lys Asn His Gln Leu Cys Thr 50 60

Glu Glu Ile Phe Gln Gly Ile Gly Thr Leu Glu Ser Gln Thr Val Gln $\epsilon 5$ 70 75 80

Gly Gly Thr Val Glu Arg Leu Phe Lys Asn Leu Ser Leu Ile Lys Lys 90 95

Tyr Ile Asp Gly Gln Lys Lys Cys Gly Glu Glu Arg Arg Arg Val 100 105 110

Asn Gln Phe Leu Asp Tyr Leu Gln Glu Fhe Leu Gly Val Met Asn Thr 115 120 125

Glu Trp Ile Ile Glu Ser 130

+1310: 234 +211: 115

+:212: PET

43133 Homo sapiens

-:400 - 234

Ile Pro Thr Glu Ile Pro Thr Ser Ala Leu Val Lys Glu Thr Leu Ala 1 5 15

Leu Leu Ser Thr His Arg Thr Leu Leu Ile Ala Asn Glu Thr Leu Arg $20\,$

Ile Pro Val Pro Val His Lys Asn His Gln Leu Cys Thr Glu Glu Ile 35 40 45

Fhe 3ln Gly Ile Gly Thr Leu Glu Ser 3ln Thr Val Gln Gly 3ly Thr 50 60

Val Glu Arg Leu Phe Lys Asn Leu Ser Leu Ile Lys Lys Tyr Ile Asp 65 70 75

Gly Gln Lys Lys Lys Cys Gly Glu Glu Arg Arg Arg Val Asn Gln Phe

Lei Asp Tyr Leu Gln Glu Phe Leu Gly Val Met Asn Thr Glu Trp Ile 100

Ile Glu Ser

C401 · 235

Met Glu Ele Pro Met Ser Thr Val Val Lys Glu Thr Leu Thr Gln Leu

Ser Ala His Arg Ala Leu Leu Thr Ser Asn Glu Thr Met Arg Leu Pro

Val Pro Thr His Lys Asn His Gln Leu Cys Ile Gly Glu Ile Phe Gln

Gly Lei Asp Ile Leu Lys Asn Gln Thr Val Arg Gly Gly Thr Val Glu

Met Leu Phe Gln Asn Leu Ser Leu Ile Lys Lys Tyr Ile Asp Arg Gln 70

Lys Gau Lys Cys Gly Glu Glu Arg Arg Arg Thr Arg Gln Phe Leu Asp

Typ Lan Gla Phe Leu Gly Val Met Ser Thr Glu Trp Ala Met Glu

 $\odot17$

%110# 236
%11 111
%112 PET
%213 Homo sapiens

-400 > 236

Ser Asp Gly Gly Ala Gln Asp Cys Cys Leu Lys Tyr Ser Gln Arg Lys 10 15

lle Pro Ala Lys Val Val Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu 25

Gly Cys Ser Ile Pro Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln 40

Ala Glu Leu Cys Ala Asp Pro Lys Glu Leu Trp Val Gln Gln Leu Met

Gin Ris Leu Asp Lys Thr Pro Ser Pro Gln Lys Pro Ala Glr Gly Jys 65 70

Arg Lys Asp Arg Gly Ala Ser Lys Thr Gly Lys Lys Gly Lys Gly Ser 95

Lys Gly Cys Lys Arg Thr Glu Arg Ser Gln Thr Pro Lys Gly Pro 100 100

ki2125 PRT

<::13 · !!us musculus</pre>

<400 - 237

Ser Asp Gly Gly Gln Asp Cys Cys Leu Lys Tyr Ser Gln Lys Lys 10 15

The Pro Tyr Ser He Val Arg Gly Tyr Arg Lys 3ln Glu Pro Ser Leu 25

Gly Cys Pro Ile Pro Ala Ile Leu Phe Ser Pro Arg Lys His Ser Lys

Pro Gla Leu Cys Ala Asn Pro Glu Glu Gly Trp Val Gln Asn Leu Met 50

Ard Arg Leu Asp Gln Pro Pro Ala Pro Gly Lys Gln Ser Pro Gly 2ys 65

Arg Lys Ash Arg Gly Thr Ser Lys Ser Gly Lys Lys Gly Lys Gly Ser 90 95

Lys Gly Cys Lys Arg Thr Glu Gln Thr Gln Pro Ser Arg Gly 110

238 .[10]

7.4

```
-126-
<21% Homo sapiens
<45) - 273
Asp Sly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe
Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn
Thr Fic Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn 40
 Arg Sin Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu
 Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
 K2100 239
K211 70
K210 PRT
         PRT
  .217 Mus musculus
  -,450 - 239
  Asp Giy Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe
  Glu Ser His Ile Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn
   The Fro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn
   Ang Gin Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu
5:
   Glu Iys Ala Leu Asn Lys
    +21C> 240
+311: 109
+312: PRT
          Homo sapiens
```

Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser 10 15

(4)) 240

Leu Sem Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg

Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile

Asp Arg The Gln Ile Leu Fro Arg Gly Asn Gly Cys Pro Arg Lys Glu ± 0

The The Val Trp Lys Lys Asn Lys Ser The Val Cys Val Asp Pro Gln

Ala Glu Trp Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser

Ser Thr Leu Pro Val Pro Val Phe Lys Arg Lys Ile Pro

<2100 241 <2110 109 <2130 PET 2F.T

1113 Mus musculus

-(400 > 241

Met Arg Leu Ser Thr Ala Thr Leu Leu Leu Leu Leu Ala Ser Cys Leu

Ser Pro Gly His Gly Ile Leu Glu Ala His Tyr Thr Asn Leu Lys Cys

Arg Cys Ser Gly Val Ile Ser Thr Val Val Gly Leu Asn Ile Ile Asp

Arg Ile Glm Val Thr Pro Pro Gly Asn Gly Cys Pro Lys Thr Glu Val 50

Val The Trp Thr Lys Met Lys Lys Val The Cys Val Asn Pro Arg Ala 80

Lys Trp Leu Gln Arg Lou Leu Arg His Val Gln Ser Lys Ser Leu Ser

Ser Thr Pro Gln Ala Pro Val Ser Lys Arg Arg Ala Ala

· 210: 242 :111 · 97

KI12/ PRT

<213 > Homo sapiens

<4(○ 240

Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala

Pho Ser Pro Gin Gly Leu Ala Gly Fro Ala Ser Val Fro Thr Thr Cys

Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser

Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe $\frac{1}{50}$

Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp $\frac{70}{60}$

Val Gin Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys

 $F \, \, r \to$

+1105 243 +111 119

-_12 - PRT .113 - Home sapiens

-:400 - 243

Mot Ala Gly Leu Met Thr Ile Vai Thr Ser Leu Leu Phe Leu Gly Val

Cys Alo Bis His Ile Ile Pro Thr Gly Ser Val Val Ile Pro Ser Pro

Cys Cys Met Phe Phe Val Ser Lys Arg Ile Fro Glu Asn Arg Val Val

Fer Tyr Gln Leu Ser Ser Arg Ser Thr Cys Leu Lys Ala Gly Val Ile 50 $\,$

Phe Thr Thr Lys Lys Gly Gln Gln Phe Cys Gly Asp Pro Lys Gln Glu 75

Trp Val Gln Arg Tyr Met Lys Asn Leu Asp Ala Lys Gln Lys Lys Ala 90 95

Ser Pro Ar; Ala Arg Ala Val Ala Val Lys Gly Pro Val Gln Arg Tyr

Fro Bly Ash Gin Thr Thr Cys 115

+10100 244 +10110 94 +10110 PRT +10110 Homo sapiens

-(4-17) - 244

Met Met Gly Leu Ser Leu Ala Ser Ala Val Leu Leu Ala Ser Leu Leu

Ser Leu His Leu Gly Thr Ala Thr Arg Gly Ser Asp Ile Ser Lys Thr

Cys Cys Fhe Gln Tyr Ser His Lys Pro Leu Pro Trp Thr Trp Val Arg

Sar Tyr Glu Phe Thr Ser Ash Ser Cys Ser Gln Arg Ala Val Ile Phe

Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His Pro Arg Lys Lys Trp

Val Gln Lys Tyr Ile Ser Leu Leu Lys Thr Pro Lys Gln Leu 85

+2100+ 245 +2110+ 37 +2112+ PFT

-213 · : Mus musculus

(4)0 - 245

Met 3ln Ser Ser Thr Ala Leu Leu Fhe Leu Leu Leu Thr Val Thr Ser

Phe Thr Ser Gln Val Leu Ala His Pro Gly Ser Ile Pro Thr Ser Cys

Cys Phe Ile Met Thr Ser Lys Lys Ile Pro Asn Thr Leu Leu Lys Ser

Tyr Lys Arg Ile Thr Asn Asn Arg Cys Thr Leu Lys Ala Ile Val Pho 50

Lys Thr Arg Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Lys Lys Trp 6°

Val Gln Asp Ala Thr Lys His Leu Asp Gln Lys Leu Gln Thr Pro Lys

Ero

.2100 246

.0110 119 .110 PRT .213 Mus musculus

.:400 - .:246

Met Ala Gly Ser Ala Thr Ile Val Ala Gly Leu Leu Leu Val Ala 10 15

Cys Ala Cys Cys Ile Phe Pro Ile Asp Ser Val Thr Ile Fro Ser Ser 25

Cys Cys Thr Ser Phe Ile Ser Lys Lys Ile Pro Glu Asn Arg Val Val

Ser Tyr Gln Leu Ala Asn Gly Ser Ile Cys Pro Lys Ala Gly Val Ile 50 $$

Ph.e Ile Thr Lys Lys Gly His Lys Ile Cys Thr Asp Pro Lys Leu Leu

Trr Val Gln Arg His Ile Gln Lys Leu Asp Ala Lys Lys Asr. Gln Pro

Sec Lys Gly Ala Lys Ala Val Arq Thr Lys Phe Ala Val Gln Arg Arg

Arg Gly Asn Ser Thr Glu Val 115

-1100- 247 -111- 553 -112- PRT -113- Homo sapiens

-(400 - 247

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu 10 15

- Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr 25
- Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu 35
- Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln 50 60
- Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys 65
- Tyr Leu Lys Lys Ala Phe Leu Leu Val 31n Asp Ile Met Glu Asp Thr 95
- Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu 100 100
- Glr. Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu 115 $\,$
- Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln 130 135
- Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu 145 150
- Asr Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala 175
- Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asr. Cys Leu 180 180
- Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His 205
- Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu 210 220
- Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Deu Pro Gly Glu Gln Fro 235 240
- Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser 255
- Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser 260 265

- Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn 275
- Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val 290 295
- Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly 305
- Thr Glu Leu Ser Pro Ser Arg Pro 3ly Gly Gly Ser Met Gln Thr 3lu 335
- Pro Ala Arg Pro Ser Ash Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala 340 345
- Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro 355
- Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro 370
- Gln Lys Th: Asp His Ero Ser Ala Lei Leu Arg Asp Pro Pro Glu Pro 385
- Gly Ser Pro Arg Ile Ser Ser Pro Arg Pro Gln Gly Leu Ser Asr. Pro 416
- Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly $425 \ \ \, 425$
- Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp 435
- Arg Arg Ser Fro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala 450 450
- Ala Arg Fro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr His 455 470 470
- Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val 485
- Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly 500
- Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln

525 520 515 Arj Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln 535 Asp Asp Arg Gln Val Glu Leu Pro Val 550 -:400 - 248 Met Thr Ala Arg Gly Ala Ala Gly Arg Cys Pro Ser Ser Thr Trp Leu Gly Ser Arg Leu Leu Val Cys Leu Leu Met Ser Arg Ser Ile Ala Lys Glu Val Ser Glu His Cys Ser His Met Ile Gly Asn Gly His Leu 4.0 Lys Val Leu Gln Gln Leu Ile Asp Ser 3ln Met Glu Thr Ser Cys Gln Ile Ala Phe Glu Phe Val Asp Gln Glu Gln Leu Asp Asp Pro Val Cys 65 Tyr Leu Lys Lys Ala Phe Phe Leu Val 31n Asp Ile Ile Asp Glu Thr Met Arg Phe Lys Asp Asn Thr Prc Asn Ala Asn Ala Thr Glu Arg Leu Gln Glu Leu Ser Asn Asn Leu Asn Ser Cys Fhe Thr Lys Asp Tyr Glu 120 115 Glu Gln Asn Lys Ala Cys Val Arg Thr Phe His Glu Thr Pro Leu Gln Leu Leu Glu Lys Ile Lys Asn Phe Phe Asn 3lu Thr Lys Asn Leu Leu 145 150 160 Glu Lys Asp Trp Asn Ile Phe Thr Lys Asn Cys Asn Asn Ser Phe Ala 170 175

- Lys Cys Ser Ser Arg Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu 180 180
- Tyr Pro Lys Ala Thr Pro Ser Ser Asp Pro Ala Ser Ala Ser Pro His 195
- Gln Pro Pro Ala Pro Ser Met Ala Pro Leu Ala Gly Leu Ala Trp Asp 210
- Asp Ser Gln Arg Thr Glu Gly Ser Ser Leu Leu Pro Ser Glu Leu Pro 240 225
- Leu Arg Ile Glu Asp Pro Gly Ser Ala Lys Gln Arg Fro Prc Arg Ser 250
- Thr Cys Gln Thr Leu Glu Ser Thr Glu Gln Pro Asn Eis Gly Asp Arg 260 265
- Leu Thr Glu Asp Ser Gln Pro His Pro Ser Ala Gly Gly Pro Val Pro 280
- Gly Val Glu Asp The Leu Glu Ser Ser Leu Gly Thr Asn Trp Val Leu 190 295
- Glu Glu Ala Ser Gly Glu Ala Ser Glu Gly Phe Leu Thr Gln Glu Ala 305 310
- Lys Phe Ser Pro Ser Thr Pro Val Gly Gly Ser Ile Gln Ala Glu Thr 335
- Asp Arg Pro Arg Ala Leu Ser Ala Ser Pro Phe Pro Lys Ser Thr Glu 340
- Asp Gln Lys Pro Val Asp Ile Thr Asp Arg Pro let Thr Glu Val Asn 365
- Pro Met Arg Pro Ile Gly Gln Thr Gln Asn Asn Thr Pro Glu Lys Thr 370
- Asi Gly Thr Ser Thr Leu Arg Glu Asp His Gln Glu Pro Gly Ser Pro 395 \$395
- His Ile Ala Thr Pro Asn Pro Gln Arg Val Ser Asn Ser Ala Thr Pro 405
- Val Ala Gln Leu Leu Pro Lys Ser His Ser Trp Gly Ile Val Leu 420 425

Pro Leu Gly Glu Leu Glu Gly Lys Arg Ser Thr Arg Asp Arg Arg Ser

Pro Ala 3lu Leu Glu Gly Gly Ser Ala Ser Glu Gly Ala Ala Arg Pro

Va: Ala Arg Phe Asn Ser Ile Pro Leu Thr Asp Thr Gly His Val Glu 470 465

Gln His Glu Gly Ser Ser Asp Pro Gln Ile Pro Glu Ser Val Phe His

Leu Leu Val Pro Gly Ile Ile Leu Val Leu Leu Thr Val Gly Gly Leu 500

Leu Phe Tir Lys Tro Lys Tro Arg Ser His Arg Asp Pro Gln Thr Leu

Asp Ser Ser Val Gly Arg Pro Glu Asp Ser Ser Leu Thr Gln Asp Glu

Asp Arj Gln Val Glu Leu Pro Val 550

<2100 249
<2111 108
<2112 FET</pre>

<213 - Homo sapiens

<400 - 249

Met Lys Ala Leu Cys Leu Leu Leu Pro Val Leu Sly Leu Leu Val

Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala lle Asn Glu Arg Tle

Gin Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly

Leu Glu Cys Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro

Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser $\frac{75}{65}$

Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met $_{\alpha \alpha}$

Asp Top Thr Gly Ala Arg Cys Cys Arg Val Gln Pro

.210 - 250 .211 - 114

PET - 212 Mus musculus

₹400 - 250

Wet Lys Asn Leu Ser Phe Pro Leu Leu Phe Leu Phe Phe Leu Val Pro

Glu Leo Leu Gly Ser Ser Met Pro Leu Cys Pro Ile Asp Glu Ala Ile

Ask Lys Lys Ile Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn Ala Ile

Lys Asn Ile Gly Leu Asn Cys Trp Thr Val Ser Ser Arg Gly Lys Leu 50

All Ser Cys Pro Glu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser

Als Dys Gly Ser Trp Asp Ile Arg Glu Glu Lys Val Cys His Cys Gln 85

Cys Ala Arg Ile Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val

Ala Ser

.1130 251 .7110 174 .112 PET .213 Homo sapiens

.400 > 251

Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln

Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu 25

Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro 35

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe

Leu Thr Sor Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro

Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg 85

Ala Pro Fro Gly Gly Gly Asp Fro Gln Gly Arg Ser Val Thr Leu Arg

Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu 125

Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala

Arg Arg 31n Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly

Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn

+210: 252 <211: 258 +212 - PRT

32.13 · Mus musculus

<400 - 252

Gln Asp Gln Gly Arg Arg Val Glu Lys Ile Ile Gly Ser Gly Ala Gln

Ila Gln Lys Arg Leu Asp Asp Ser Lys Pro Ser Cys Ile Leu Pro Ser 20

Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg Leu His Pro Gln Arg

Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser Gln Gly Pro Val Ala 55

Gin Ser Ser Arg Glu Ala Ser Ala Trp Met Thr Ile Leu Ser Pro Ala

Ala Asp Ser Thr Pro Asp Pro Gly Val Gln Gln Leu Pro Lys Gly Glu 85

Pro Glu Thr Asp Leu Asn Pro Glu Leu Pro Ala Ala His Leu Ile Gly 100

Ala Trp Met Ser Gly Gln Gly Leu Ser Trp Glu Ala Ser Gln Glu Glu

Ala Pho Leu Arg Ser Gly Ala Gin Phe Ser Pro Thr His Gly Leu Ala

Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys His Val Gly Tyr Arg 150

Gly Ar; Thr Pro Pro Ala Gly Arg Ser Arg Ala Arg Ser Leu Thr Leu

Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Arg Gly Ser Pro 130

Glu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Val Asp Fro

Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Li0 -215

Ala Gin Leu Arg Ser Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro 230

Asp Met Val Asp Tyr Arg Arg Gly Lys Thr Phe Phe Gly Ala Val Met

Val Gly

+111 + 255 +111 + 128 +111 + PRT +111 + RNA-phage PP7

-:40J · 253

Met Ser Lys Thr Ile Val Leu Ser Val Gly Glu Ala Thr Arg Thr Leu

Thr Glu Ile Gln Ser Thr Ala Asp Arg Gln Ile Phe Glu Glu Lys Val

Gly Pro Leu Val Gly Arg Leu Arg Leu Thr Ala Ser Leu Arg Gln Asn

- Gly Ala Lys Thr Ala Tyr Arg Val Asn Leu Lys Leu Asp Gln Ala Asp
- Val Val Asp Cys Ser Thr Ser Val Cys Gly Glu Leu Pro Lys Val Arg
- Tyr Tor Cln Val Trp Ser His Asp Val Thr Ile Val Ala Asn Ser Thr
- Giu Ala Ser Arg Lys Ser Leu Tyr Asp Leu Thr Lys Ser Leu Val Ala
- Thr Ser 3ln Val Glu Asp Leu Val Val Asn Leu Val Pro Leu Gly Arg
- kC12 · FRT
- #213 * FNA-phage SP A1 protein
- 41400 254
- Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly Asp
- 31n Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly Val
- Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
- Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys Val
- Gir. The Lys Leu Gir Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys Asp
- Pr: Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe Thr
- Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu Ala
- Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu Asn
- Pro Ala Tyr Trp Ala Ala Leu Leu Val Ala Ser Ser Gly Gly Gly Asp 130 135

Asn 145	Pro	Ser	Asp	Pro	Asp	Val	Pro	Vāl	Val	Pro 155	Asp	Val	Lys	Pro	Prc 160
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- Asp Bly Thr Gly Arg Tyr Lys Cys Pro Phe Ala Cys Tyr Arg Leu Gly
- Ser Ile Tyr Glu Val Gly Lys Glu Gly Ser Pro Asp Ile Tyr Glu Arg
- Gly Asp Glu Val Ser Val Thr Phe Asp Tyr Ala Leu Glu Asp Phe Leu
- Gly Asn Thr Asn Trp Arg Asn Trp Asp Gln Arg Leu Ser Asp Tyr Asp
- Ile Ala Asn Arg Arg Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp 230 235
- Ala Thr Ala Met Gln Ser Asp Asp Phe Val Leu Ser Gly Arg Tyr Gly
- Val Arg Lys Val Lys Phe Fro Gly Ala Phe Gly Ser Ile Lys Tyr Leu 260
- Leu Asn Ile Gln Gly Asp Ala Trp Leu Asp Leu Ser Glu Val Thr Ala
- Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser
- Pro Gin Leu Pro Thr Asp Phe Thr Gln Phe Asn Ser Ala Asn Cys Pro 310
- Val Gin Tor Val Ile fle Ile Pro Ser Leu
- +210+ 255 +211+ 132 +212+ PRT

- -212 PRT -213 Qb 240
- :400 253
- Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys
- Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val 25

Ala Ser Leu Ser Gl
n Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val3%

Th: Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val 50

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys 75 70

Asp Fro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe 85

The Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu 100 100

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp 3ln Leu 115

Asn Pro Ala Tyr 130

.210> 25€

·:11: 132 ·:212 · PF.T

-213 - Qb 243

-(400)> 256

Ala Lys Leu Glu Thr Val Thr Leu Gly Lys Ile Gly Lys Asp Gly Lys 1 5 $$

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val 20 30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val 35

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val 50 55

Glr. Val Lys Ile Gln Asn Fro Thr Ala Cys Thr Ala Asn Gly Ser Cys 75

Asy Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe 85 90

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu 100 100 Ala Ala Leu Leu Ala Ser Pro Leu Leu lle Asp Ala Ile Asp Gln Leu

Asn Fro Ala Tyr 130

-213> Qb 250

<400 → 257

Ala Arg Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Arg Asp Gly Lys

Gir. Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val

Ala Ser Leu Ser Gln Ala Gly Ala Val Fro Ala Leu Glu Lys Arg Val

The Val. See Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val

Glm Val Lys Ile Glm Asm Pro Thr Ala Cys Thr Ala Asm Gly Ser Cys

Ask Prc Ser Val Thr Arg Gln Lys Tyr Ala Ask Val Thr Phe Ser Phe

Thr Gir. Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu

Ali Ali Lou Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu 115

Ash Fro Ala Tyr 130

- 110: - 258 - 11: - 132 - 112: - FFT -113: - Qp 259

<400 → 25€

Ala Arg Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Arg 5

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val 25

Ala Ser Leu 3er Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val 35

Thr Vai Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val 50 50

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys 75 70

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe 95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu 100 105

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu 115 126 125

Asn Pro Ala Tyr 130

₹400 - 259

Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Arg
1 10 15

Oln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val 20 25

Ala Ser Leu Ser Gl
n Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val\$45\$

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val 50

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys 75 70 80

Asp Pro Ser Val Thr Arg Gln Lys Tyr Ala Asp Val Thr Phe Ser Phe 95

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The Blo Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
           1.00
Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
115
Asn Fie Ala Tyr
    130
AUTO 200
-111 10
-111 EMA
-111 Artificial Sequence
 x 2.20
 .l... FH19 primer
                                                                                20
 4400× 165
 tabytector goodogtaco
 -.200 -
.200 - PH30 primer
                                                                                 20
  - 455× 261
  tagasarras gotoacttoo
  .210% 262
kill - 31
kill - 101A
kill - Artificial Sequence
   .510 .
.5.3 . 8881 primer
                                                                                  30
   4 . . . 163
   Typus'scyg gatgaagaac ctttcatttc
   - 110 - 163
- 111 - 31
- 111 - TNA
- 113 - Artificial Sequence
    PH22 primer
                                                                                   31
    14 14 243
    inititagag aggaagegae etgeagetta e
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46
ctarraged ggggtggatg tggggacgac tacaaggatg acgaca
14 4 6 4 L 4 4
.016 - 065
.011 - 46
.010 - DMA
.013 - Artificial Sequence
 1215 FHEE primer
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 <310 * 160
<311 * 45
<310 * 5MA
<310 * Artificial Sequence</pre>
  45
  agettactica cacatgodda cogtgoddag cacctgaago cgagg
  +2108 267

*2118 36

+2124 EWA

2138 Artificial Sequence
   .2235
.2235 PH32 primer
   38
   - 216 - 168
- 211 - 27
- 212 - 2NA
- 212 - Artificial Sequence
   -210 · - 9835 primer
                                                                                   37
    411 - 268
    attainidad ggggtggatg tgggatcgaa ggtcgca
    269

211 - 37

211 - DNA

211 - Artificial Sequence
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.::: PH36 primer
                                                                                         37
1. 4 · 1. · 1. · 1. · 15 P
application of togatocc acatecacco ectedog
Public 270
Poils 43
Poils UNA
Poils Artificial Sequence
43
 4400 - 270
 chigatical cagetggget egaggtgeta getttgttta aac
 0010 0 071
0011 0 05
0011 0 DNA
0013 0 Artificial Sequence
 <!d00 | |
<!-- EH38 primer</pre>
                                                                                           55
  datingtitua acaaacaaag ctagcaccte gagcccaget getggatede ggtac
  OBION 272
OBION 57
OBION CMA
OBION Artificial Sequence
  37
   430 - 272
   ctagogaga ggggtggatg tggggacgat gacgaca
   CITE 273
CITE 37
CITE EMA
CITE Antificial Sequence
   .210.
2.1. FH40 primer
                                                                                             37
     11.14 273
    ancingtogt categiocce acatecaded detectog
    001100 274
001110 30
00110 ENA
00110 Artificial Sequence
     Alls. PH41 primer
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kiji - 274 dalijisusta gadadadtod tgotatgggt	30
R. 19 - 135 R.11 - 19 R.11 - ENA R.11 - Artificial Sequence	
<pre>.010 .010 .013 - EH40 primer .400 - 075 .grantacoda tagbaggagt gtgtotgtot coatggtac</pre>	39
<pre> .111 · 176 .111 · 17 .111 · 1NA .112 · Artificial Sequence .113 · Artificial Sequence .113 · Artificial Sequence .114 · Artificial Sequence .115 · Artificial Sequence .115 · Artificial Sequence .116 · Artificial Sequence .117 · Artificial Sequence .118 · Art</pre>	
.DDG - CDD38 PH43 primer C4008 D76 actgotgoto tgggttocag gttocactgg tgacgcg	37
<pre>%210 * 277 %211 * 36 %212 * INA %213 * Artificial Sequence</pre>	
<pre>kll0 * kll2 * 1844 primer k400 * 277 gatorgogto accagtggaa cotggaacco agagca</pre>	36
-110	
.110. .111. SU7 primer .41078 .420. i78	40
RING 279 RIII 40 RIII 5 DNA RIII 6 Artificial Sequence	
 : SM8 primer .::: 279 .;:::cactot agaacotoga googatatoo tggatoogoa	40

<210> 280

+00110 107 +00120+ PEC -01130 Mus musculus

<400 ← 280

Ser Ser Met Pro Leu Cys Pro Ile Asp Glu Ala Ile Asp Lys Lys Ile

Lys Gln Asp Phe Asr Ser Leu Phe Pro Asr. Ala Ile Lys Asn Ile Gly

Leu Asr. Cys Trp Thr Val Ser Ser Arg Gly Lys Leu Ala Ser Cys Pro

Glu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser Ala Cys Gly Ser

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Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val Ala Ser Ser Leu

Ala Gly Gly Gly Cys Gly Ile Glu Gly Arg

<210> 281
+211> 107
+212> PRT
+213> Mus musculus

.:400> 281

Ser Ser Met Pro Leu Cys Pro Ile Asp Glu Ala Ile Asp Lys Lys Ile

Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn Ala Ile Lys Asn Ile Gly

leu Asn Cys Trp Thr Val Ser Ser Arg Gly Lys Leu Ala Ser Cys Pro 35

Flu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser Ala Cys Gly Ser 50

Trp Asp Ile Arg Glu Glu Lys Val Cys His Cys Gln Cys Ala Arg Ile 65 70 80

Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val Ala Ser Ser Leu Ala Bly Gly Gly Gly Cys Gly Asp Asp Asp Asp +210+ 082 +001+ 103 +011+ PET <001+ Mus musculus <400 - 280</p> Ser Ser Met Fro Leu Cys Pro Ile Asp Glu Ala Ile Asp Lys Ile 1 5 Lys Gl: Asp Phe Asn Ser Leu Phe Pro Asn Ala Ile Lys Asn Ile Gly Let Asr. Cys Trp Thr Val Ser Ser Arg Gly Lys Leu Ala Ser Cys Pro 35. $46\,$ Glu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser Ala Cys Gly Ser The Asp Ile Arg Glu Glu Lys Val Cys His Cys Gln Cys Ala Arg Ile 80 Asc Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val Ala Ser Ser Leu Ala Gly Gly Gly Gly Cys Gly 283 10233 LNA · 13 · Artificial Sequence -:110 -:13 pCer-Xa-Fc construct -2.0 --311 - misc feature -131 - (9820)..(9820) -323 - n is a, c, g, or t goomsgoogo oggaegaadt aaaddtgadt acggdatdto tgddddttot togdtggtad 60 ..:01 - 283

gagyagngot titigititigi attoggggoa gigsatgiaa tooottoagi iggitiggias 120

180 aacttgocaa otgggoontg ttocacatgt gabanggggg gggabbaaac acaaaggggt tototyactg tagttgabat cottataaat ggatutgcac atttgccaac actgagtggc 24:) 301 tttbatcotg gagoagastt tgoatgotgt ggad.gsaac acaacattgs cittatgigt aactottggo tgaagititt acaccaatgo tggg:gacat gtacctocca guggoocagu 360 aagactacgg gaggotacac baacgtraat cagagagago tgtgtagota bugataagog 42.7 gaccotcaag agggcattag baatagtgtt tataaggobb oottgttaab obtaaacggg 4 € tagratatgo ttoorgggta gtagtatata otatroagao taaoortaat traatagoat 540 6:: atgttaccca acgggasyca tatgctatcg aattagggtt agtaasaggg toctaaggas 6...: cagogatato toccacocca tgagotgtca oggititatt tabatggggt caggattoca ogagggtagt gaaccanttt agtoacaagg goagt ggotg aagatoaagg agogggoagt 7_0 gaaststoot gaatsttoge etgettette attimisente gtitagetaa tagaataast 760 $\in \mathbb{T}^{1}$ gotgagttgt gaadagtaag gtgtatgtga ggtgotogaa aadaaggtet baggtgadgd occcagaata aaattiggad gggggttda gtggtggdat tgtgdtatga dacdaatata 900 adopticacaa accopinggg caataaatab taqtqtagga atgaaabatt otgaatatot (0,0)ttaacaatag aaatersitgg ggtggggaca agesgtaaag actggatqtc catctsacac 1000 gaatttatgg otatgggcaa cacataatoo tagtgcaata tgatactggg gttattaaga 1000 tgtgtcccag gcagggacca agacaggtga acratgttgt tacactctat ttgtaacaag 1140 gggaaagaga gtggacgecg acageagegg acteraetgg ttgtetenaa eacececqaa 1..:: 1260 aattaaacgg ggotocacgo caatqgggco cataaacaaa gacaajtggo cabtottttt 1331 titgaaattg tggaqtgggj geacgegtea gebreeaeae geogeoetge ggittitggae tgtaaaataa gggtgtaata asttggotga ttgtaacccc gctaaccact gcggtcaaac 1391 capttgooca caasardact astgqoacoo oqqqqaatac otgrataagt aqqtqqqoqq 1440 goraagatag gggryngatt gotgrgatot guanqadaaa ttadabacada ttgcgootga 1460 gegodaagda caggyttgtt qytdotoata thewbqaggt cqctgajage aeggtgqget C astyttycca tyggtagcat atactaccca aututotyga tagcatatyc tatcctaatc 1.560 tatatotggg tagnataggo matootaato tatatotggg tagoatatgo tatootaato tatatotggg tagtatatjo tatootaatt tatatotggg tagcataggo tatootaato 1...:0 tatatotggg taglatatgo tatootaato tatatotggg tagtatatgo tatootaato 18.0 1960 tytatocygy tajsatatys tatoctaata yagattajyy tajtatatys tatostaatt tatātotggg tagoatatāc taopoaaata totggatago atatgotato otaatotata 1920 totgggtage atatgotato etaatetata totgggtage ataggotate etaatetata 1980

2741 totgagtago atatgotato otaatotata totaggdtagt alatgotato otaattitata 2:11 totyjgtago ataggotato otaatotata totgggtago atatgotato otaatotata totgygtayt atatgotato otaatotgta toogggtago atatgotato otoatgoata () () 1.1.37 tacagtcago atatgataco cagtagtaga gtgpgagtgo tatectttgo atatgregeo 1. + 1 accteopaag ggggogtgaa tittogetge tigioettit eetgeatgot ggtitgeloe: attettaggt gaatttaagg aggeeagget aaajeegteg eatgtetjat tgetekeeag 1340 1400 gtaaatqtog staatgtitt sommoqogag maqqtqttqa gogoggaqot gagtquogtq adascatggg tatgoccast tgpcccatgt tgggaggacg aaaatggtga caagacagat ..4 (31) ggrsagaaat ababbaabag babgbatgat gtotabtggg gatttattst ttagtgbggg 1910 0.930 ggaatacacg gottittaata ogattigaggg ogtotoctaa caagittacat cactootigco ottootsago otoateteda teacetoett datataegte ateteegtea teacesteag (4.40) eggeagreed ttecaceata ggtygaaace aggyaggeaa atetacteea tegteaaage 1790 37€0 tgracacagt caccotgata tigdaggtag gagogggott tgtrataaca aggirottaa tegeattett caaaaoetea geaastatat gajtttgtaa aaagaetstg aaatsataja 3-10 .. 5 50 daatgpacto pottagoggo obaggttgtg ggoogggtoo aggggooatt ocaaliggga gaogactoaa tggtgtaaga ogacattgtg gaatagbaag ggbagttbot ogobttaggt 2341 tgtaaaggga ggtottacta ootobatata ogaabacado ggogabocaa gttoottogt 3010 31,60 eggtagtoot ttotaegtga eteotageea ggagagetet taaaeettet geaatgttet caaattuogy gttygaacot oottgaccae gatyotttoo aaaccacoot oottitttyo 3125 2130 gootgrates athaceetga opengaggte cagtgentag goottetect gagtsatetg 3049 eggggeretg etstateget ecegggggca egtcaggets accatenggg ecansitistt 3300 guitgutatto aasataatog gottoocota cagggiggaa aaatugoott otaustggag guagostaca caqtaugada cauqutqata atquestact astqquanto atquestat 1.460 titiotocapg topacgadot otopocotgg coofficacg actificade otggetofft 14.0 :4-0 caegitostat audzeggegg ectebadiad etestogado eeggeetosa etaeutosta gasocoggic tipactgoot cotogascoo quistocaco testquiost geometestg 5540 chartgeala technologic pergeocote elgebecche tachectace deresingue ·:)0 . € € 0 stantyptod typopotoot genaptooty steetypeed teatypeed detectyets stgsscatas tgccsctaat estgataatg accetsstga acatsstgat actgascata :"20 stgeceated tgetsetged detectgede etdetgeted tgseesteet getaalgede :..80 etantgetee tgeceeteet getectgese etectgenee testgeceet estestgete 1540

3911 atgracater typications retractigate etanlyrade testgatect caccateste atgatantga septoatque astantgode etda estga testquesat catquesate 39. 1 4000 ctditgator typodectout dotablocty popularty additionage contestably etertagees tretages of catestapte etaphestoc testagement presentations 4 (-) codetestge coetootest got sitgeed atostoutge teatgessot satisfessote 4145 etgeocetes tycocetect estactecty decetestes tyctostyce setsetyets 7 otgeometre egotoetget cotgetentg streasingty gateentity ragematique 4. (1) 4320 aanttygang tittiggggt otolgganan batcintatg totiggroot gatootgage egopogyggo toetggtett eegroteete gteet/gtee totteeregt eetegteeat 4 460 4440 ggttatoard deptotottett tgaggtroad tgoogeogga geostotggt ocagatgtgt officialities tootaggica titucaggic officareting constructs garatgatic 4500 4550 acactaaaag agatcastag acatctttat tajacgacgo toagtgaata cajaggagtgo agactuotgo occeteraad agroecessa ecotoatese ettoatggto getqtsagae 4.600 $\mathbb{L}_{+}:=\{i\}$ agateraggit etgassatte eccathetec gasecaterit egioricate armaattaet 4740 ogdagloogg aaaactooog otgaacatoo toaagattig ogtoitgago otdaagooag gostcaaatt octogtocco chittigsty gargetaqyy atggggatto togggascoc 4800 teotettiet ettiaaggte aepagaeaga gatgetaetg gggeaaegea aacaigagaa 4360 4,320 ttottgaaga ogaaagggos togtgataog obtattitta taggstaatg toatgataat 4330 aatgatttot tagaogtoag grigoacttt togaggasat gtgegoggas eocctatttg $\Xi \cap A \, (t)$ tttättttto taaatacatt osaatatgta toopotoatg agadaataab ootgataaat gottomaataa tattomaamaa gomaajagtat gagtattomaa sattooogto tojoocttat 5100 5160 tedestitust geggeatiti geoliosigi tittigetead ecagaaaege tgytgaaagt : ÷ assagatget gaaganeagt tiggitijsaeg agtijggttae atersacter atmesacag eggtaagate ottqujagtt ttegeocoga isaaegtttt ocaatgatga geaettttaa -.290 5.540 agitotypta tgtqyogogg tattatodog tyttgacgod gagcaagayo aactoggtog 1400cogratacae tattotoaga atgaettegt tyagtaotea coagtoacag aaaageatet 1460 tadyganggo atgabagtaa magaattatq bagtgotgod atwaccatga yigataadad 5520 tgo jgo saac ttarttotga raa sqategg aggaed jaag qayotaacig shttittigea paabatgygg gateatgtaa utugeottga tegttgygaa degyagetga atgaagebat 5580 5640 accaaacgad gagogtgada headgatdoo tgbagdaatg gdaacaacgt tgcgbaaact attaactggc gaaltactta ctstagctts ocjącaacaa ttaatagact ggatggaggc 5700

5761 ggataaagtt geaggaceae ttetgegete gjeeetteng getggetggt ttattgetga taaatotgga googgtaago gtaggtotog oggtatoatt goagnaotgg ggooagatag 58.11 5831 taagoootoo ogtatoqtay ttatotadad gacqgggayt baggdaacta tygatgaabg aaatagacag atogotqaga taggtgooto actgattaag cattggtaac tgtcagacca 5 4 6.00 agittactca tatata itti agattgatti aasacttjat tittaattta aaaggatota ggtgangato ettittgata atotoatqae Gaaaaticeet taabgtgagt tittegitidea 6.11. 1 otgagogtoa gaccocgtag asaagatcaa aggatottot tgagatoott titittotgog (\cdot,\cdot,\cdot) ogtaatistgo tgottucasa saanaaa.co aeegetasca geggtgybtt gttigseyga €; : .) toaagagota scaactetet teesgaaggt aastggeete agcagagoge agataccaaa 6241 £3 05 tactgroott otagtgtage cytagttagg ocadeactte aagaactetg tageacegod 6360 tacatacete getetgetaa teetgttass amtggetget gecagtqqeg ataaqteqtg tottacoggg tiggacicaa gacqatagti acoggataag gogcagoggi ogggotgaac 4420 6480 gyggggttog tgcacacago reagettgga gogaacdade tacacegaac tgagatacet $\rho_{1} \in A_{2}(\cdot)$ acagegtyag statyagaaa gogecasgot teorgaaggg agaaaggogg acaggtatec 6600 ggtsajogge agggteggaa baggagageg cacqaqigag ettocagggg gasaegestg grateritat agreetging ygttingena enterganti gagngingat tirtgigatg $\vec{v}_i,\vec{v}_i \in \mathbb{N}$ ctcgtcaggg gggrggagec tatggaaaaa bqcragcaac goggcotttt tacogstoot €720 ggoottttge tgcqccqcgt gcqqctqctq qaqatqqcgg acqcqatqga tatqttctgc $\mathcal{C} \not \in \mathcal{G}$ caagggttgg tittgogbatt cabagttoto ogcaagaatt gattggetod aattottgga 6040 6900gtigotgaato ogitagogag godatobago otogogtoga abtagatgat oogbigtigga $\mathcal{C} \cong \mathcal{C}(0)$ atytytytoa yttagyytyt gyaaaytooo cayyotoooc aycaggoaga aytatysaaa -- : .: 0 goatgoatot caattagtoa goaaccaggt gtggaaagto cobaggetee coagcaggea 715.50 gaagtatgca aagsatgcat cicaaitaqt caqcaaccat agtccopocc ctaactoogo destroeged estasetee; obdastterg posstletee gronnatgge tysetsattt 140 $C \ni \mathbb{T}^n$ thtitattita tgcagaggos gaggicyost iggoshotga gotattodag aagtagtgag - ...60 gaggotttit toqaqqqtga toqonabqad byqtysbqbd accatboost qabbbadqdd collgapoost cacaaggaga ogacitticoa tiqaiogagta caagessaog qtgegioteg . :20 .380 ccarcogoga oglogtopes ogggongtad gnarbotogo ogdogogtto godgaptado 7440 cogedacçey doasacegte gadeoogade gosacatega acqeqteace gagetgoaag 7500 aactottoot cacgogogto gggotogada toggoaaggt gtgggtogog gadjacggog 7560 ocgoggtggo ggtotggaec acgloggaga gogtogaago gggggeggtg ttogoogaga

7620 teggecegng catggengay ttgageqqtt eeeggetgge egegeageaa cagatggaag gootootaja googoajegg oocaagjago oogoqtggtt ootqqooaco gtojgoqtot 765-1 egeoogadia deagggiaag ggtotgjgok gegeegtogt geteooligga gtggaggegg 77.: . degagegige eggggtjirr goettertji ajachteege gedeegeaae etrosettit 73:1 73() abgagogget oggettuade gteacogody abglegagtg ecogaaggab ogegogaest 7920 ggtgbatjad dogbaajobe ggtgbotgab gccogeodda ogabbeqbag egebegabog aaaggagogo acgaccoyqt oogacqgcqg cocabgqgto bbaqggqqgt ogacctoqaa 79-0 acttgtttat tgcagottat aatggttaca aataaaqcaa tagcatcaca aatttcacaa 8040 ataaagcatt tittteactg cattolagit gtggttigto casactoatc aatgtatott 8111 atcatgining gategating association togaccasts ofcatgining acadestate 8160 81110 atograyato ogggcaacyt tgtigcaiig otgcagyogo agaactyyta gytatggaay atotatadat tyaatossta tigydastia yodstattag toathygtia tatagdataa 8080 atbaatattg gotattggod attgcalabg ttglatbtat atcalaatat gtabatttat 3340 attggotoat gtocastatg accgoodigt tgasattgat tattgactag trattaatag 8400 taatcaatta oggggslatt agstoatago odatatatgg agstoogogt tacataactt 8460 85..0 acggtasatq geochertgg etgaccheed aabgaeeded geocattgae gteaataatg angtatqtto ocatagnaac godaataggg actiticatti garqtiaatg ggtggagtat 81390 ttacggtaaa otgoocsott ggcagtabat casgtgtate atatgbcaag toogcoocst $\gamma \in 4 \cup$ attgacqtca atgacqutaa atqqcccqcc tqqcattatq cccaqtacat qascttacqq 5700 gaotitoota oftggoagta datotabyta ttagtdatog otattacbat ygtgatyogg $\geq 7 \in \mathbb{Q}$ tettgycagt acaccastgg geytggatag eggtttgact caeggggatt tocaagtete 9 ÷ 30 cappointing acquesatgy paytitizett tggcappaaa atcaacggga officeaaaa 8-80 tgtogtaata approjedop githachdas anggeoggia geogligiadg giteggageth 2.34 . [] tatataagoa gaget/gttt agtgaseogt cagateteta gaagetgggt acegggatoo (i) agcagotggg ctowargtgo tagoggjagg gggtggatgt ggdatogaag gtogcaagot 21.0 tactoscaca tyc magacyt ghodaydaco tyaagoogay ggygbacogt bagtottoot 11:0 ottonoccea adamicaagg ababeltoat gatonoccgg accostgagg teacangogt jątyjtygas giganicaeg aagasisiga gątsaagito aasiggiaeg tyjasygegi -240 ggaggtgoat aatgiisaaga saaagsiggog ggaggagcag talaacagca igtanogtgt 3:0 ggtcagogtc otcarogtoc tgcaccagga otgcotgaat ggcaaggagt acaagtgcaa 1360 ggtotocaan aaagmeetee cageeteeat egagaaaaes atotocaaag ecaaagggea 3420

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gailestigg cagooggaga acaactacaa gaccacgoot coogtyttyg actoogacgg
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ctintinto ototacagea ageteacegt ggacaagage aggtggcage aggggaaegt
                                                                      97.0
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                                                                      97-0
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                                                                      9840
atacattyat gagttiggac aaaccacaac tagaatgcag tgaaaaaaat gctttattig
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 tquadatttit gatgetattg etttatttgt aaccattata agetgeaata aacaagttaa
 caa macaan tigoattoatt ttatgittoa ggttoagggg gaggtgggga ggttttttaa (1901)
 adimagtama acototacaa atgtggtatg gotgattatg atcoggotgo otogogogtt
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 tanaaauga tgoogggago agadaagood gtoagggoo gtoagogggt gttggogggt 10000
                                                                      10133
 groggagoga agocatgaco ggtogactot aga
 +210 + 284
+211 + 19
+202 + 5MA
+213 + Artificial Sequence
 +210 -
+213 - 5'LT oligonucleotide primer
                                                                          19
  3 : 4
  ottggtgong baggatbag
  .210% 285
   .211 - 13
         Artificial Sequence
  .223. 3'LT oligonucleotide primer
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   1400 - 135
   ragariggity teaccecae
          136
-7
          .. NA
          Artificial Sequence
   ..... A'LT long-NheI oligonucleotide primer
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grisgotago etgeggtggt caggateagg gaegteg	37
*.13 * 287 *.111 * 37 *.112 * DNA *.113 * Artificial Sequence	
.220. .223 - 5'LT short-NheI oligonucleotide primer	
-4000- 257 greegotage otgoggtggt totocagotg oggatto	37
10: 258 11: 33 10: EMA 13: Attificial Sequence	
.220 .220 : LT stop-NotI oligonucleotide primer	
.400 - 188 paatgadigo ggoogottad occapdatda oog	33
S010 - 089 -111 - 504 -0100 PRT -0120 Artificial Sequence	
<pre>.010DOB - GST-EK-C-LT fusion protein</pre>	
(100 × 189	
Ala Pro Leu Val Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly 10 15	
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr 20 25	
Glo Glo His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys 35	
Type Pho Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp	
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala 65 75 80	
Asi Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile 95	
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg	

110 105 100 Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser 120 Lys Leu Pro Glu Met Leu Lys Met Fhe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Pne Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Fhe Fro Lys Leu Val Cys Fhe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Ieu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln 195 Gly Trp Gln Ala Thr Fhe Gly Gly Gly Asp His Fro Pro Lys Ala Ser Met Thr Gly Gly Gln Glr Met Gly Arg Asr Leu Tyr Asp Asp Asp Asp Lys Leu Ala Cys Gly Gly Gln Asr Gln Gly Arg Arg Val Glu Lys Ile Ile Gly Ser Gly Ala Gln Ala Gln Lys Arg Leu Asp Asp Ser Lys Fro Ser Cys lle Leu Pro Ser Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro 280 285 Arg Leu His Pro Gln Arg Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser Gln Gly Pro Val Ala Gln Ser Ser Arg Glu Ala Ser Ala Trp Met 310 305 Thr Ile Leu Ser Pro Ala Ala Asp Ser Thr Pro Asp Pro Gly Val Gln 335 Gln Leu Pro Lys Gly Glu Pro Glu Thr Asp Leu Asn Pro Glu Leu Pro 340 Ala Ala His Leu Ile Gly Ala Trp Met Ser Gly Gin Gly Leu Ser Trp

Glu Ala Ser Gln Glu Glu Ala Phe Leu Arg Ser Gly Ala Gln Phe Ser

Pro Thr His Gly Leu Ala Leu Pro Gin Asp Gly Val Tyr Tyr Leu Tyr 390

Cys His Val Gly Tyr Arg Gly Arg Thr Pro Pro Ala Gly Arg Ser Arg

Ala Arg Ser Leu Thr Leu Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala

Tyr Gly Arg Gly Ser Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val

Thr Pro Val Val Asp Pro Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser 455

Val Sly The Gly Sly Leu Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr

Val Asn Ile Ser His Pro Asp Met Val Asp Tyr Arg Arg Gly Lys Thr 485

Fhe Fhe Gly Ala Val Met Val Gly 500

+0100 290 +0110 427 +012 PRT

. 113 Artificial Sequence

-1220

0.223 - GST-EK-C-LT fusion protein

430 - 290

Ala Fro Leu Val Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly

Leu Val Gln Pro Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr

Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys

- Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ilo Asp 55
- Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala 65
- Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile $\frac{35}{35}$
- Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg 100
- Ile Ala Tyr Ser Lys Asr Phe Glu Thr Leu Lys Val Asp Phe Leu Ser 125
- Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asr Arg Leu Cys His Lys 130 135
- Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr 145
- Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala 175
- Fhe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln 180
- The Asr Lys Tyr Leu Lys Ser Ser Lys Tyr The Ala Trp Pro Leu Gln 195
- Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ala Ser 210
- Met Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp 240 225
- Lys Leu Ala Cys Gly Gly Ser Pro Ala Ala Asp Ser Thr Fro Asp Pro 255
- Gly Val Gln Gln Leu Pro Lys Gly Glu Pro Glu Thr Asp Leu Asn Pro 265
- Glu Leu Pro Ala Ala His Leu Ile Gly Ala Trp Met Ser Gly 3ln Gly 275
- Leu Ser Trp Glu Ala Ser Gln Glu Glu Ala Phe Leu Arg Ser Gly Ala 290 295

- Gln Phe Ser Pro Thr His Gly Leu Ala Leu Pro Gln Asp Gly Val Tyr 310 305
- Tyr Leu Tyr Cys His Val Gly Tyr Arg Gly Ang Thr Pro Pro Ala Gly
- Arg Ser Arg Ala Arg Ser Leu Tor Leu Arg Ser Ala Leu Tyr Arg Ala
- Gly Gly Ala Tyr Gly Arg Gly Ser Pro Glu Leu Leu Glu Gly Ala
- Gla Thr Val Thr Pro Val Val Asp Pro Ile Gly Tyr Gly Ser Leu Trp
- Tyr Thr Ser Val Gly Fhe Gly Gly Leu Ala Gln Leu Arg Ser Gly Glu 390
- Ang Val Tyr Val Asm The Ser His Pro Asp Met Val Asp Tyr Arg Arg
- Gly Lys Thr Phe Phe Gly Ala Val Met Val Gly 420
- <3100 231
- <211 311
- < 312 > PFT
- <213 Artificial Sequence
- \cdot 220 \cdot kis-myc-EK-C-LT fusion protein k123 \times his-myc-EK-C-LT
- 4.400 > 291
- Ala Pro Leu Val His His His His His Gly Pro Leu Val Asp Val 10 10
- Ala Ser Asn Glu Glr. Lys Leu Ile Ser Glu Glu Asp Leu Ala Ser Met
- Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys 45
- Leu Ala Cys Gly Gly Gln Asp Gln Gly Ang Arg Val Glu Lys Ile Ile
- Gly Ser Gly Ala Gln Ala Gln Lys Arg Leu Asp Asp Ser Lys Pro Ser 65

Cys Ile Leu Pro Ser Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg 85

Leu His Pro Gln Arg Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser 100 100

Gln Gly Pro Val Ala Gln Ser Ser Arg Glu Ala Ser Ala Trp Met Thr 115

Ile Leu Ser Pro Ala Ala Asp Ser Thr Pro Asp Pro Gly Val Gln Gln 130

Leu Pro Lys Gly Glu Pro Glu Tnr Asp Leu Asn Pro Glu Leu Pro Ala 145 150 150

Ala His Leu Ile Gly Ala Trp Met Ser Gly Gl
n Gly Ieu Ser Trp Glu\$170\$

Ala Ser Gln Glu Glu Ala Pho Leu Arg Ser Gly Ala Gln Phe Ser Pro 185 190

Thr His Gly Leu Ala Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys 195

His Val Gly Tyr Arg Gly Arg Thr Pro Fro Ala Gly Arg Ser Arg Ala 210 215

Arg Ser Leu Thr Leu Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr 235 230

Gly Arg Gly Ser Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr 250 245

Pro Val Val Asp Pro 11e Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val 260 265

Gly Phe Gly Gly Lea Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr Val 285

Asn Ile Ser His Pro Asp Met Val Asp Tyr Arg Arg Sly Lys Thr Phe 290

Fhe Gly Ala Val Met Val Gly 305

<210> 1192 <211> 234 <2120 PET

<213> Artificial Sequence

:::220F

+223: his-myc-EK-C-LT fusion protein

<400 · 292

Ala Pro Leu Val His His His His His Gly Pro Leu Val Asp Val

Ala Ser Asn Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Ala Ser Met

Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys $\frac{35}{40}$

Leu Ala Cys Sly Gly Ser Pro Ala Ala Asp Ser Thr Pro Asp Pro Gly

Val Gln Gln Leu Fro Lys Gly Glu Pro Glu Thr Asp Leu Asn Pro Glu $\epsilon = 70$

Leu Pro Ala Ala His Leu Ile Gly Ala Trp Met Ser Gly Gln Gly Leu

Ser Trp Glu Ala Ser Glu Glu Glu Ala Phe Leu Arg Ser Gly Ala Gln

Phe Ser Pro Thr His Gly Leu Ala Leu Pro Gln Asp Gly Val Tyr Tyr

Leu Tyr Cys His Val Gly Tyr Arg Gly Arg Thr Pro Pro Ala Gly Arg 130 135

Ser Arg Ala Arg Ser Leu Tor Leu Arg Ser Ala Leu Tyr Arg Ala Gly 145

Gly Ala Tyr Gly Arg Gly Ser Pro Glu Leu Leu Leu Glu Gly Ala Glu 175 165

Thr Val Thr Pro Val Val Asp Fro Ile Gly Tyr Gly Ser Leu Trp Tyr

Thr Ser Val Gly Fhe Gly Gly Leu Ala Gln Leu Arg Ser Gly Glu Arg 195

Val Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Tyr Arg Arg Gly 210 220

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Lys The The Phe Gly Ala Val Met Val Gly 2:5
.222. MOS-1F oligonucleotide primer
                                                                         43
. 4mm - 193
tatagationg getagogete gagggtttaa aeggeggeeg eat
 +316 + 334
+211 + 45
+311 + 55A
+313 + Artificial Sequence
 45
 togastycky cogoogitta aaccotogag ogotagoogg atoca
 %110 * ..95
%110 * E8
%110 * EMA
%213 * Artificial Sequence
  % CLGS
% Eamhis6-EH-Nhe-F oligonucleotide primer
                                                                          58
  patienaire accaedadea chaeggitet ggigacgaeg aigacaaage gelageed
  .210 - 236
.231 - 58
         /.rtificial Sequence
   Size Samhis6-EK-Nhe-R oligonucleotide primer
   transports gegettigte ategtegtea ceagaacegt ggtggtggtg gtggtgtg
                                                                           58
   . ;⊕. - . 96
   .::A. : 197
.::1. 42
.::1. DNA
.::. Artificial Sequence
    ..:::: 297
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110 10 10 110 110 110 110 110 110 110 1	t ::::::::::::::::::::::::::::::::::::	42
-400 - 198 garagetht aaacttatta accgcaacca ccaccaccac cc 42 -110 - 199		
110 135 111	: Ligo1R-C-glycine-linker	42
### Artificial Sequence ###################################	ggoogogettt aaacttatta acegeaacea eeucoott - 110 - 193 - 111 - 81 - 111 - 1NA	
togaggatas aacccacac totocgccgt gtggttaata agtttaaccg c 110	.110 Artificial Sequence .110113 - olago1F-C-gamma1-linker	-1
### Artificial Sequence #### Artificial Sequence ##################################	togaqqataa aacocacaco totoogoogi geggeedd in g	51
-400 - 300 groupsttt aaacttatta accacacggc ggagaggtgt gggttttatc c -210 - 201 -211 - 201 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 204 -211 - 205	<pre>%.ld DNA %.ld Artificial Sequence %.ld Artificial Sequence</pre>	
2113 - Artificial Sequence 2113 - Artificial Sequence 2113 - Cligo1Fa-C-gamma3-linker 240 - S01 2513 - Cligo1Fa-C-gamma3-linker 210 - S02 211 - S8 211 - INA 2113 - Artificial Sequence 21 - Cligo1RA-C-gamma3-linker		51
36 10 13 12 23 a acceptatace degeographic cttety 10 10 10 20 2 111 10 28 111 10 10 10 10 10 10 10 10 10 10 10 10		
L10 + 302 - 111 + 58 - 112 + 1NA - 112 + Artificial Sequence - 22 + 1 - 113 - 11golRA-C-gamma3-linker		36
::	L10 - 202 - 711 - 78 - 773 - INA	
'': "''''	.22 	38

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39
attationed aggragation ggttaataag titaaacgo
1466 - 303
-211- 304
-211- 27
-212- 5MA
-213- Amorficial Sequence
 - 115
- 115 - Oligo2RB-C-gamma3-linker
                                                                                 37
 <4\%\,30.4
 phocacutt aaacttatta accgcaacca cooggag
 AJ10 - 305
AJ11 - 39
AJ108 DBA
D13 - Artificial Sequence
  - 1225-
- 1... rMIF-F oligonucleotide primer
                                                                                 33
  .400 - 305
  ggaattocat atgoctatgt toatogtgaa cac
  C110 + 306
+111 + 19
+111 + ENA
+113 + Artificial Sequence
   .:::::
_:::: rMIF-C1 oligonucleotide primer
                                                                                   29
   .; · · · 316
   recartegag agogaaggtg gaaccgtto
   .::: 307
.::: 124
.::: FFT
.::: Artificial Sequence
    rMIF-C1 protein
    4:324 307
    Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro
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- Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly 2.0
- Lys Fro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met
- Thr Pho Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser 55
- 115 Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu 65 70 75
- Cys 3'y Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr
- Tie Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser
- Thr Fne Ala Leu Glu Gly Gly Gly Gly Cys Gly

- + 11) + 308 + 111 + 127 + 312 + PET + 113 + Artificial Sequence
- + DDO +
 +.DD3 + rMIF-C2 protein
- .,4: (+ 398
- Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro
- Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly
- Lys Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met
- Tr.r Phe Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser
- Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu 75 80
- Cys Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr

Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser 100

Thr the Ala Leu Glu Asp Lys Thr His Thr Ser Pro Pro Cys Gly

-2.10 - 309 .:211 - 1.35

VIII PPT VIII Artificial Sequence

-:220 -

:213 rMIF-C3 protein

904800 × 309

Met Pro Met Ehe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro

Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly

Lys Pro Ala Glr. Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met

Thr Phe Ser 3ly Thr Ser Asp Fro Cys Ala Leu Cys Ser Leu His Ser

Tie Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu 6°.

Cys Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr

ll. Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser

Thr Fne Ala Leu Glu Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly 120 115

Oly Ala Pro Gly Gly Cys Gly

· 110: 310

- 111: 124

-_12'- PRT ...13 · Homo sapiens

-:400 - 310

Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro

1	5	10	15
Asp Gly Phe Leu	Ser Glu Leu T	hr Gln Gln Leu Ala G 25	ln Ala Thr Gly 30
Lys Pro Fro Gln	Tyr Ile Ala V	Val His Val Val Fro A	sp Gln Leu Met
35		40	5
Ala Phe Gly Gly	ser Ser Glu : 55	ero Cys Ala Leu Cys (60	Ser Leu His Ser
ile Gly Lys Ile	e Gly Gly Ala	Gln Asn Arg Ser Tyr .	Ser Lys Leu Leu
	70	75	80
Cys Gly Leu Le	u Ala Glu Arg	Leu Arg Ile Ser Fro	Asp Arg Val Tyr
	85	90	95
Ile Asn Tyr Ty	r Asp Met Asn	Ala Ala Asn Val Gly	Trp Asn Asn Ser
10	O	105	110
Thr Fhe Ala Le	eu Glu Gly Gly	Gly Gly Gly Cys Gly 120	
<pre><2150 311 <2110 123 <212 PFT <213 Home s</pre>	apiens		
<400 ⋅ 311			
Pro Met Phe I	le Val Asn Thr	r Asn Val Pro Arg Ala	Ser Val Pro Asp
	5	10	15
Gly Phe Leu S	Ser Glu Leu Thi	r Gln Gln Leu Ala Glr 25	Ala Thr Gly Lys 30
iro Pro Gln '	ryr Ile Ala Va	l His Val Val Pro Asp	Gln Leu Met Ala
35		40	45
Phe Gly Gly	Ser Ser Glu Pr	to Cys Ala Leu Cys Se	r Leu His Ser Ile
50	55	60	
Gly Lys Ile	Gly Gly Ala Gl	In Asn Arg Ser Tyr Se	r Lys Leu Leu Cys
	70	75	80
Gly Leu Leu	Ala Glu Arg Le	eu Arg Ile Ser Pro As	sp Arg Val Tyr Ile
	85	90	95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr

Phe Ala Leu Glu Gly Gly Gly Gly Cys Gly

40.100 312 40.11 127 40.11 PRO

:::13 · Homo sapiens

<400 . 312

Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro

Ask Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly

Lys Fro Pro Glr Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met 35

Ala Pho Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser

Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu 70

Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr

Ile Asn Tyr Tyr Asr Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser

Int Fae Ala Leu Glu Asp Lys Thr His Thr Ser Pro Pro Cys Gly 120

·210: 313

-111 126 -112 PRT -113 Homo sapiens

::00 - 313

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys

Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala

Fhe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 75 70

Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr

Fig. Ala Leu Glu Asp Lys Thr His Thr Ser Pro Pro Cys Gly 125

.213 - PFT

4213 · Homo sapiens

(400) > 314

Met Pro Met Fhe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro

Ask Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly

Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met

Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser 50 55

Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu 75 80

Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr

Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser 100 100

Thr Phe Ala Leu Glu Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly 125

Gly Ala Pro Gly Gly Cys Gly 130	
#210% +15 #211% 134 #211% FRT #21% Homo sapiens	
0400 - 715 Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp 10 1	
Sly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 25	
Fr. Pr: Glr. Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala 40 45	
Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50	
Gly Lys Ite Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 65	
Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile 90 95	
Ast. Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr 100 100	
Fig Ala Leu Glu Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Gly 125	
Ala Pro Bly Cly Cys Gly 330	
- 110 - 316 - 111 - 62 - 112 - DNA - 115 - Artificial Sequence	
- 22) - RANKL-UP oligonucleotide primer	
-40] - 316 stgssagggg esegggtgeg geggtggeda teateaceae cateaceage getteteagg	60 62
эg	

-:210> 317

35

+211 35 +212 DNA +211 Artificial Sequence RANYL-DOWN oligonucleotide primer - in: - 317 especegagt tagtetatgt cetgaacttt gaaag .010 318 .010 419 .010 PRT .010 Artificial Sequence ALLES Protein of GST-PS-C-FANKL ₹450 - 316 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Th: Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 Gly Leu Glu Fhe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Len Asn 130 Oly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Fro Gln Ile Asp Lys Tyr
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Glu Val Leu

Phe Gln Gly Pro Gly Cys Gly Gly Gly His His His His His Eis Gln 240

Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val 250

Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile 265 270

Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser 275 280 285

Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asr Met Thr Leu Ser 290 295

Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Fhe Tyr Tyr Leu Tyr Ala 320

Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp 330 335

Tyr Leu Gin leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro 345

Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly 365

Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys 370

Leu Arg Ala Sly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu 385 390 390

Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln 405 410

Asp Ile Asp

+:210 · 319 <:211 · 1269 1212 L :NA Artificial Sequence 3220 H +C213+ CDNA sequence of GST-PS-C-RANKL atgreeceta tactaggita tiggaaaatt aagggeetig igeaacceae tegaciteti -60 ttygaatato ttyaagaaaa atatgaagag catttytaty agogogatga aggtgataaa 170 tggcgaaaca aaaagtttga attgggtttg gagtttooca atottootta ttatattgat 184 ggtgatgtta aattaacaca gtotatggoo atcatacgtt atatagotga caagcacaac 2.1 . atattgggug gtuguccaaa agagogugba gagatttcaa ugcutgaagg agoggtutug 30: gatattagat acggigtite gagaattgea tatagtaaag actitgaaac teleaaagtt 360 gailttetta geaagetace tyaaatgetg aaaatgtteg aagategttt atgteataaa 420 asatatttaa atgytyatoa tytaacosat ootgacttoa tyttytatya ogotstigat 480 grightitat acanggacoc aangngoong gangoghnoo caaaannagn thighthhaaa 连耳0 assogtatty asyctatocc acasattyst sagtacttys astecaycas gratiatages 6.0tygoottige agggetggea agoeacgitt ggiggiggeg accateetee asaateggat 66... ctqjaajtto tgttooaggg gooogggtge ggoggtggee atcatcacca coatcaccag 7...) 790 egetteteag gagetocage tatgatgyaa ggeteatggt tggatgtgye esagegagge aagootgagg cocagocatt tgcacacotc accatcaatg otgocagoat obsatogggt (::3 $G \subseteq \mathbb{C}$ tocca aaag toactotgto stottggtad dacgatogag gotgggccaa gatototaad stiacittaa qoaacggiaa actaaqggtt aaccaagatg gottotatta cotgtacgoo $9 \in \mathbb{C}$ sanatitgot ttoggoatoa tgaaadatog ggaagogtad otadaganta tottdagotg 14.0 atggt statg togttaaaac cagcatcaaa atcccaagtt stcataacct gatgaaagga 1 ...[1140 ingag acga aaaactggto gggcaattot gaattocact titattocat aaatgttggg quattitica ageteegage tggtgaagaa attageatte aggtgtesaa ceetteestg 1. 0 1...50 riggatoogg atcaagatgo gaogtacttt gggggotttoa aagttoagga catagactaa 1:59 ntogagogg

_10 320

^{...11 - 185}

^{- 112} PRT

<213. Artificial Sequence

<:220>

:223: Human-FANKL construct

<400 - 320

Sly Cys Sly Gly Gly Gln His Ile Arg Ala Glu Lys Ala Met Val Asp

Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro

Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His

Lys Tal Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile

Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly 70

Fhe Tyr Tyr Leu Tyr Ala Asn Ile Cys Fhe Arg His His Glu Thr Ser

Gly Asr Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys 100

Th: Ser Ile Lys Ile Pro Ser Ser His Tar Leu Met Lys Gly Gly Ser

Thr Lys Tyr Trp Ser Gly Asr. Ser Glu Fhe His Phe Tyr Ser Ile Asn

Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu 1.1.

Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe

Gly Ala Phe Lys Val Arg Asp Ile Asp 180

321 - 2.10:-

29

DNA

Artificial Sequence

:223 · 5'PrP-BamHI oligonucleotide primer

<400> 321

c;//gatecca ceatggtggg gggeettgg	29
<pre></pre>	
- 220 · - 228 · 3'PrP-NheI oligonucleotide primer	
<pre><400 + 322 otagotages tggatettet deeg</pre>	24
+310 + 323 +311 + 350 +311 + 7FT +331 + Artificial Sequence	
127 Protein sequence of mPrPt-EK-Fc	
. 400 · 3.23	
Met Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg 10 15	
Fro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr Tyr Arg Glu 20 25	
Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln 35	
Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Ile 50	
Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu 65	
Th. Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met Cys Val Thr 95 85	
Gla Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg Ser Arg Leu 105	
Ala Gly Gly Gly Cys Gly Asp Asp Asp Asp Lys Leu Thr His Thr 115 120 125	
Tys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe 13)	
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro	

145	150	155	j.	160
Glu Val Thr Dys Val	Val Val Asp	Val Ser His	s Glu Asp Pro	Glu Val 175
Lys Phe Asn Trp Tyr 180	Val Asp Gly	Val Glu Va. 135	l His Asn Ala 190	Lys Thr
Lys Pro Ard Glu Gla 195	Gln Tyr Asn 200	Ser Thr Ty	r Arg Val Val 205	Ser Val
Leu Thr Val Leu His 210	s Glr. Asp Trp 215) Leu Asn Gl	y Lys 3lu Tyr 220	r Lys Cys
Lys Val Ser Asn Lys 205	s Ala Leu Pro 230	o Ala Ser Il 23	le 31u Lys Th 35	r Ile Ser 240
Lys Ala Lys Gly Gl 24	n Pro Arg Gli 5	u Pro Gln Va 250	al Tyr Thr Le	u Pro Pro 255
Ser Arg Asp Glu Le 260	u Thr Lys As	n Gln Val S 265	er Leu Thr Cy 27	vs Leu Val 70
Lys Gly Phe Tyr Pr 275	o Ser Asp Il 28	e Ala Val G 80	lu Trp Glu Se 285	er Asn Gly
Gln Pro Glu Asn As 200	sn Tyr Lys Th 295	nr Thr Pro E	Pro Val Leu A. 300	sp Ser Asp
Gly Ser Phe Phe L 305	eu Tyr Ser Ly 310	ys Leu Thr '	Val Asp Lys S 315	er Arg Trp 320
Cin Tin Gly Asn V 3	al Pho Ser C 25	ys Ser Val 1 330	Met His Glu A	Ala Leu His 335
Asn His Tyr Thr G 340	ln Lys Ser L	eu Ser Leu 345	Ser Pro Gly I	Lys 350
02100 324 -2110 124 -211 FRT -113 Artificial	l Sequence			
-120 - -123 - Protein s	equence of m	PrPt		
-:400 - 324				
Met Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg				

15 10

Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr Tyr Arg Glu

Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln

Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Ile

Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu

Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met Cys Val Thr

Gin Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg Ser Arg Leu 105

Ala Gly Gly Gly Cys Gly Asp Asp Asp Asp Lys

- 2100 335

.311 - 102

.212 PRT .113 Artificial Sequence

- 310 e

s.203> Human F.esistin-C-Xa construct

4400 → 325

Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile

Glr. Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ilo Ser Ser Ile Gly

Leu Glu Cys Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro 35

Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser

Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met 75 75

Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro Gly Gly Gly

95 90 85

Cys Gly Ile Glu Gly Arg

*21. * 326 *211 * 103 *217 * PET *222 * Artificial Sequence

+220 + + + Human Resistin-C-EK construct

4999 326

Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile

Glr. Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly 20

Lea Gla Cys Glr. Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro 35

Ar; Gly Fhe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser

Try Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met

Ask Ter Thr Gly Ala Arg Cys Cys Arg Val Gln Pro Gly Gly Gly

Cys Gly Asp Asp Asp Asp Lys 100

+ 110: 327 + 111 + 98 + 112 + PET + 113 + Artificial Sequence

. 120 -__3 - Human resistin-C construct

100 · 327

Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile 1 5

Gin Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly 25

Leu Glu Cys Gin Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro 35 40 45

Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser 50 60

Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met 55 70 75 30

Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro Gly Gly Gly Gly

cys Gly

·:..10. 32.8

+111 + 132 +1112 + PRT +1113 + Artificial Sequence

+223 - mouse C-IL-13-F protein

-1400 - 318

Arg Ser Val Ser Leu Pro Leu Thr Leu Lys Glu Leu Ile Glu Glu Leu

Ser Asn Ile Thr Gln Asp Gln Thr Pro Leu Cys Asn Gly Ser Met Val 35 40 45

Trp Ser Val Asp Leu Ala Ala Gly Gly Phe Cys Val Ala Leu Asp Ser

Leu Thr Asn Ile Ser Asn Cys Asn Ala Ile Tyr Arg Thr Gln Arg Ile ± 5 70 75 80

Leu His Gly Leu Cys Asn Arg Lys Ala Pro Thr Thr Val Ser Ser Leu 85 90 95

Pro Asp Thr Lys Ile Glu Val Ala His Phe Ile Thr Lys Leu Leu Ser

Tyr Thr Lys Gln Leu Phe Arg His Gly Pro Phe Leu Glu Val Leu Ala 115 120 125

Ile Glu Gly Arg 130

+01100 329 +01110 119 +0110 PRT

Artificial Sequence

Modse C-IL-13-S protein

<400 ← 329

Let Ala Cys Gly Gly Gly Gly Gly Pro Val Pro Arg Ser Val Ser

Leu Ero Leu Thr Leu Lys Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr

Glm Asp Glm Thr Pro Leu Cys Asn Gly Ser Met Val Trp Ser Val Asp

Leu Ala Ala Gly Gly Phe Cys Val Ala Leu Asp Ser Leu Thr Asn Ile 50 55

Ser Asn Cys Asn Ala Ile Tyr Arg Thr Gln Arg Ile Leu His Gly Leu

Cys Asn Arg Lys Ala Pro Thr Thr Val Ser Ser Leu Pro Asp Thr Lys

Ile Glu Val Ala His Fhe Ile Thr Lys Leu Leu Ser Tyr Thr Lys Gln 105

Let Fhe Arg His Gly Pro Phe 115

+ 2100 - 330

+0110 133 +0120 PRT +013 Artificial Sequence

- 111 - Human C-IL-13-F protein

:450 + 330

Ala Asp Pro Gly Cys Gly Gly Gly Gly Leu Ala Gly Pro Val Pro 1 5

Pro Ser Thr Ala Leu Arg Glu Leu Tle Glu Glu Leu Val Asn Ile Thr 20 30

Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile 35 40 45

Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn 50 60

Val Ber Gly Cys Ser Ala Ile Blu Lys Thr Gln Arg Met Leu Ser Gly

Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser Leu His Val

Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu

His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Leu Glu Val Leu

Ala Ile Glu Gly Arg

+:210:- 331

+12:11: 12:0 +12:12: PF.T

+12131 Artificial Sequence

+13201+

Human C-IL-13-S protein

+14001 3.51

Leu Ala Cys Gly Gly Gly Gly Gly Gly Pro Val Pro Pro Ser Thr Ala 1 5 10 15

Let Arg Glt let The Glt Glt Let Val Asn The Thr Gln Asn Gln Lys 20 -25

Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala

Gry Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys 50 60

Ber Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His

Lys Val Ser Ala Gly Gin Pne Ser Ser Leu His Val Arg Asp Thr Lys 85 90 95

Ile Glu Val Ala Gln Phe Val Lys Asp Leu Leu His Leu Lys Lys 105

Lou Phe Arg Glu Gly Arg Phe Asn 115

- 1.10 332
- ·111 · 136
- 1.12 PRT
- 113 Artificial Sequence
- · . .30 ·
- ·123 · Mouse C-IL-5-E protein
- +400 332

Ala Leu Val Gly Cys Gly Gly Pro Lys Pro Ser Thr Pro Pro Gly Ser I 5 10 15

Ser Gly Gly Ala Pro Ala Ser Met Glu Ile Pro Met Ser Thr Val Val 20 25

Lys Glu Thr Leu Thr Glr. Leu Ser Ala His Arg Ala Leu Leu Thr Ser

Asi. Glu Thr Met Arg Leu Pro Val Pro Thr His Lys Asi His Gli Leu

Cys lle Gly Glu Ile Phe Gln Gly Leu Asp Ile Leu Lys Asn Gln Thr

Val Arg Gly Gly Thr Val Glu Met Leu Phe Gln Asn Leu Ser Leu Ile

Lys Lys Tyr Ile Asp Arg Gln Lys Glu Lys Cys Gly Glu Glu Arg Arg

Ard Thr Arg Gln Phe Leu Asp Tyr Leu Gln Glu Phe Leu Gly Val Met

Jer Thr Glu Trp Ala Met Glu Gly

- +:210:+ 333 +:211:+ 134 +::12:+ PRT +:213:+ Artificial Sequence

<22.00 €

<223. Mouse C-IL-E-F protein

H400N 333

Ala Asp Pro Gly Cys Gly Gly Gly Gly Leu Ala Met Glu lle Pro 1 10

Met Ger Thr Val Val Lys Glu Thr Leu Thr Gln Leu Ser Ala His Arg

Ala Leu Leu Thr Ser Asn Glu Thr Met Arg Leu Pro Val Pro Thr His

Lys Asn His Gln Leu Cys Ile Gly Glu Ile Phe Gln Gly Leu Asp Ile ± 0 ± 0 ± 0

Ash beu Ser Leu Ile Lys Lys Tyr Ile Asp Arg Gln Lys Glu Lys Cys

G y Glu Glu Arg Arg Arg Thr Arg Gln Phe Leu Asp Tyr Leu Gln Glu

Phe Deu Gly Val Met Ser Thr Glu Trp Ala Met Glu Gly Leu Glu Val

Leu Ala Ile Glu Gly Arg 130

%:110:+ 3:4
*:011:+ 1:1
*:012:+ PET
*:113:+ Artificial Sequence

-1.1201-

H. 25H Mouse C-IL-5-3 protein

-14000 334

Leu Ala Cys Gly Gly Gly Gly Met Glu Ile Pro Met Ser Thr Val

Val Lys Glu Thr Leu Thr Gln Leu Ser Ala His Arg Ala Leu Leu Thr

Ser Asn Glu Thr Met Arg Leu Pro Val Pro Thr His Lys Asn His Gln 35 40 45

Leu Cys Ile Sly Slu Ile Phe Sln Sly Leu Asp Ile Leu Lys Asn Sln 50 60

Thr Val Arg Sly Gly Thr Val Glu Met Leu Phe Gln Asn Leu Ser Leu 65 70 75 80

The Lys Lys Tyr Ile Asp Arg Gln Lys Glu Lys Cys Gly Glu Glu Arg 85 90 95

Arg Arg Thr Arg Gln Phe Leu Asp Tyr Leu Gln Glu Phe Leu Gly Val $100 \,$ $105 \,$ $110 \,$

Met Der Thr Glu Trp Ala Met Glu Gly 115 120

-:210:- 335

1.11 138

-1. 121- PRT

+1213: Artificial Sequence

+12/2/01+

Human C-IL-5-S protein

-14001- 335

Ser Gly Gly Ala Pro Ala Ser Ile Pro Thr Glu Ile Pro Thr Ser Ala 20 25 30

Lou Val Lys Glu Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu Leu 35 40 45

The Ala Asn Giu Thr Leu Arg Ile Pro Val Pro Val His Lys Asn His 50 55 60

3 n Leu Tys Thr Glu Glu Ile Phe Gln Gly Ile Gly Thr Leu Glu Ser 60°

G.n Thr Val Gln Gly Gly Thr Val Glu Arg Leu Phe Lys Asn Leu Ser 85 90 95

Leu Ile Lys Lys Tyr Ile Asp Gly Gln Lys Lys Lys Cys Gly Glu Glu 100 105 110

Arg Arg Arg Val Asn Gin Phe Leu Asp Tyr Leu Gin Glu Phe Leu Gly 115 120 125

"al Met Asn Thr Glu Trp Ile Ile Glu Ser 130 135

- +:017> 336
- +0.110 136 +0.110 PRT
- H213: Artificial Sequence
- 1203 · Human C-IL-5-F protein
- ·(4)) · 336
- Ala Asp Pro Gly Cys Gly Gly Gly Gly Leu Ala Ile Pro Thr Glu
- Ile Pro Thr Ser Ala Leu Val Lys Glu Thr Leu Ala Leu Leu Ser Thr
- His Arg Thr Leu Leu Ile Ala Asn Glu Thr Leu Arg Ile Pro Val Pro
- Val His Lys Asn His Gln Leu Cys Thr Glu Glu Ile Phe Gln Gly Ile
- Gly Thr Leu Glu Ser Gin Thr Val Gln Gly Gly Thr Val Glu Arg Leu
- Phe Lys Asn Leu Ser Leu Ile Lys Lys Tyr Ile Asp Gly Gln Lys Lys 8.5
- Lys Cys Gly Glu Glu Arg Arg Arg Val Asn Gln Phe Leu Asp Tyr Leu 105 100
- Gln Glu Phe Leu Gly Val Met Asn Thr Glu Trp Ile Ile Glu Ser Leu
- Glu Val Leu Ala Ile Glu Gly Arg 130

- +210: 337 +211: 123 +112: PRT -13: Artificial Sequence
- 0110 -
- 313 Human C-IL-5-S protein
- -:400.· 337
- Leu Ala Cys Gly Gly Gly Gly Ile Pro Thr Glu Ile Pro Thr Ser 10
- Ala Leu Val Lys Glu Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu 25 30

```
Leu Ile Ala Asn Glu Thr Leu Arg Ile Pro Val Pro Val His Lys Asn
His 3ln Leu Cys Thr 3lu Glu Ile Phe Gln Gly Ile Gly Thr Leu Glu
     50
                            55
Ser Jln Thr Val Gln Gly Gly Thr Val Glu Arg Leu Phe Lys Ash Leu
                       70
                                              75
Ser Leu Ile Lys Lys Tyr Ile Asp Gly Gln Lys Lys Lys Cys Gly Glu
311 Arg Arg Arg Val Asn 31r Phe Leu Asp Tyr Leu Gln Glu Phe Leu
                                    105
Gly Val Met Ash Thr Glu Trp Ile Ile Glu Ser
Hullo + 338
Hullo + 27
Hullo + DNA
Hullo + Artificial Sequence
42237
-.. 2: - NheIL13-F oligonucleotide primer
440 : 338
otamotamos gggddggtgd daagatd
                                                                                 27
c. 1600 339
cd1100 26
kd1100 PNA
cd1100 Artificial Sequence
\% \ 200 \times \ \% \ \Sigma h \oplus T E 13-R oligonucleotide primer
339 B
titorogagg aaggggoogt ggogaa
                                                                                 26
HILLS 340
HILLS 55
HILLS DNA
HILLS Artificial Sequence
+021.50 Spelinker3-F1 oligonuolestide primer
+400: 340
moodgooggg tioticiggo ggigoicogg biagoaigga gailbobaig aguab 55
<210> 341
```

```
+:011% 5.3
1111 - DNA
4...13 Artificial Sequence
· 1.1.1.1 · ·
-002 - OpeNlinker3-F2 bligbnucleotide primer
9(40) 9 341
                                                                                   52
titiactaen tggttgoggo ggoodgaaac ogagdaccoo googggttot to
HO10+ 340
HO11+ 40
HO11+ DNA
HO15+ Artificial Sequence
+02 +
+...13 + 11/0StopXho-R oligonucleotide primer
titiqogado gogtitadas togagitati ageoticoat igeocacio
                                                                                  49
$3108 343
$1117 15
$0117 bttA
$1117 Artificial Sequence
----- BanH1-FLK1-F oligonucleotide primer
3 4 1 5 5 5 1 1 1 4 1 5
progratica tidatogost otgic
                                                                                   25
SULTON 344
SULTON DEA
SULTON DEA
SULTON Artificial Sequence
* [ _ _ ] | [ - ]
-0.73- Nh.e1-FLK1-B oligonucleotide primer
-1400 j 344
Standaget Etgtgtgaac toggac
                                                                                   26
+0.100+ 545
+0.10+ 0.05
+0.10+ PRT
+0.10+ Artificial Sequence
4000 345
Pro Phe Ile Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr
Glu Ash Lys Ash Lys Thr Val Val Ile Fro Cys Arg Gly Ser Ile Ser
```

20 25 30

Asn Leu Asn Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val 35 40 45

Pro Asp Gly Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu

Pro Ser Tyr Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys 65 70 75 80

Ile Asn Asp Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val

Gly Tyr Arg Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu

Leu Ser Ala Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu 120

Leu Asn Val Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser

His His Lys Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr

Val Ala Lys Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys

Ser Asp Gln Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile 180 185 190

Lys Arg Asn Arg Thr Phe Val Arg Val His Thr Lys Pro 195 205

02100 346
02110 263
02120 PET

<213> Homo sapiens

-:4001- 346

Leu Ala Cys Gly Gly Gln Asp Gln Gly Arg Arg Val Glu Lys Ile Ile

Gly Ser Gly Ala Gl: Ala Gli Lys Arg Leu Asp Asp Ser Lys Ert Ser 20 25 30

Dys Ile Leu Pro Ser Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg

Leu His Pro Gln Arg Ser Asn Ala Ser Arg Asn Lou Ala Ser Thr Ser 55

Gin Gly Pro Val Ala Gin Ser Ser Arg Glu Ala Ser Ala Trp Met Thr

Ile Leu Ser Pro Ala Ala Asp Ser Thr Pro Asp Pro 3ly Val Gln 3ln

Leu Pro Lys Gly Glu Pro Glu Thr Asp Leu Ash Pro Glu Leu Pro Ala

Ala His Leu Ile Gly Ala Trp Met Ser Gly Sin Gly Leu Ser Trp Glu

Ala Ser Gln Glu Glu Ala Phe Leu Arg Ser Gly Ala Gln Phe Ser Pro 130 135

Thr His Gly Leu Ala Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys 1.45

His Val Gly Tyr Arg Gly Arg Thr Pro Pro Ala Gly Arg Ser Arg Ala

Arg Ser Leu Thr Leu Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr

Gly Arg Gly Ser Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr 195 200

Pro Val Val Asp Pro Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val

Gly Phe Gly Gly Leu Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr Val 235 235 240

Ash The Ser His Pro Asp Met Val Asp Tyr Arg Arg Gly Lys Thr Pho 245 250 25

Phe Gly Ala Val Met Val Gly 260

<210> 347
<211> 186

KA125 PRT

<213 → Homo sapiens

<400 - 347

Len Ala Cys Gly Gly Ser Pro Ala Ala Asp Ser Thr Pro Asp Pro Gly
1 10 15

Val Gln Gln Leu Pro Lys Gly Glu Pro Glu Thr Asp Leu Asn Pro Glu 20 25 30

Let Pro Ala Ala His Leu Ile Gly Ala Trp Met Ser Gly Gln Gly Leu 35 40 45

Ser Trp Glu Ala Ser Gln Glu Glu Ala Phe Leu Arg Ser Gly Ala Gln 10 55 60

Low Tyr Cys His Val Gly Tyr Arg Gly Arg Thr Pro Pro Ala Gly Arg 85 90 95

Ser Arg Ala Arg Ser Leu Thr Leu Arg Ser Ala Leu Tyr Arg Ala Gly 100 105 110

G.y Ala Tyr Gly Arg Gly Ser Pro Glu Leu Leu Glu Gly Ala Glu 115 120 125

Thr Wal Thr Pro Wal Val Asp Pro Ile Gly Tyr Gly Ser Leu Trp Tyr 130 135

Thr Ser Val Gly Phe Gly Gly Leu Ala Gln Leu Arg Ser Gly Glu Arg 145 150 155 160

Val Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Tyr Arg Arg Gly 165 170 175

Lys Thr Phe Phe Gly Ala Val Met Val Gly 180 185

-11101- 348

111: 117

-01120- PRT

Artificial sequence

12201-

(223) Modified human prion protein fragment

<400> 348

Val Sly Gly Leu Gly Sly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro 1 5 10 15

Ile Ile His Pne Gly Ser Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn

Met His Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Met Asp Glu Tyr

Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Ile Lys

Gin His Thr Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr

Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln

Tyr Glu Arg Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Arg Leu Ala Gly 100 105 110

Gly Gly Gly Cys Gly 115

-1210.- 349

H211 + 117

-1212.- PRT

+0.7130 Artificial sequence

 $< 0.0200 \cdot$ $< 0.0230 \cdot$ Modified bovine prion protein fragment

-400: 349

Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro

Leu Ile His Phe Gly Ser Asp Tyr Giu Asp Arg Tyr Tyr Arg Glu Asn

Met His Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln Tyr

Wer Ash Gln Ash Ash Phe Vai His Asp Cys Val Ash Ile Thr Val Lys

Glu His Thr Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr 65 70 75

Asp Ile Lys Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln 90

Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Arg Leu Ala Gly 110

Gly Gly Cys Gly $11\bar{5}$

+3210 + 350 +3211 + 117 +212 + PET

213 · Artificial sequence

· ...20 -

<2230 Modified sheep prion protein fragment</pre>

<4000 350</pre>

Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro 10 15

Leu Ile His Phe Gly Asn Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn

Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Arg Tyr

Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Val Lys 55

Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr 70 75

Asp Ile Lys Ile Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln 85 90

Tyr 3ln Arg Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Arg Leu Ala Gly

Gly Gly Gly Cys Gly 115